

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:54:16 ; Search time 83 Seconds
(without alignments)
47.167 Million cell updates/sec

Title: US-09-674-913A-1

Perfect score: 19
Sequence: 1 NVPEHERMGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Size : 0

Total number of hits satisfying chosen parameters: 5709

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database :

SPRMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5	26.3	14	11 Q920G5	Q920G5 mus musculus
2	4	21.1	17	4 Q16310	Q16310 homo sapien
3	4	21.1	17	4 Q13376	Q13376 homo sapien
4	4	21.1	19	4 Q16271	Q16271 homo sapien
5	4	21.1	20	11 Q90U21	Q90U21 mus musculus
6	3	15.8	10	2 P83067	P83067 rattus sp.
7	3	15.8	10	2 Q8RSU1	Q8RSU1 helicobacte
8	3	15.8	10	10 P82937	P82937 hordeum vul
9	3	15.8	10	11 Q9QVE7	Q9QVE7 rattus sp.
10	3	15.8	10	11 Q9QVE8	Q9QVE8 mus sp. pro
11	3	15.8	10	11 Q9QVE7	Q9QVE7 mus sp. pro
12	3	15.8	11	3 Q90R95	Q90R95 pichia angu
13	3	15.8	11	4 Q60614	Q60614 homo sapien
14	3	15.8	11	4 Q9NR38	Q9NR38 homo sapien
15	3	15.8	11	5 P83321	P83321 penaeus mon
16	3	15.8	11	5 Q9VN99	Q9VN99 drosophila

17	3	15.8	11	5 P82698	P82698 leucophaea
18	3	15.8	11	6 Q9TRW5	Q9TRW5 bos taurus
19	3	15.8	11	10 Q04131	Q04131 lycopersico
20	3	15.8	11	10 Q99N81	Q99N81 mus musculus
21	3	15.8	11	11 Q921H5	Q921H5 mus musculus
22	3	15.8	11	12 Q89616	Q89616 avian infec
23	3	15.8	11	15 Q9D232	Q9D232 human immun
24	3	15.8	11	16 Q9K744	Q9K744 bacillus ha
25	3	15.8	12	2 Q50303	Q50303 bacillus st
26	3	15.8	12	2 Q9R5E7	Q9R5E7 helicobacte
27	3	15.8	12	2 Q9R5E5	Q9R5E5 helicobacte
28	3	15.8	12	6 Q9TRT8	Q9TRT8 bos taurus
29	3	15.8	12	6 Q9X531	Q9X531 sus scrofa
30	3	15.8	12	10 Q8SAS2	Q8SAS2 pinus sylve
31	3	15.8	12	11 Q9QZD0	Q9QZD0 mus musculus
32	3	15.8	12	11 Q61331	Q61331 mus musculus
33	3	15.8	12	12 Q69232	Q69232 bovine herp
34	3	15.8	13	2 Q55234	Q55234 synecocyst
35	3	15.8	13	2 Q47693	Q47693 escherichia
36	3	15.8	13	4 Q9UM46	Q9UM46 homo sapien
37	3	15.8	13	7 Q29823	Q29823 homo sapien
38	3	15.8	13	8 Q9XLI2	Q9XLI2 bemisia tab
39	3	15.8	13	8 Q9T2U1	Q9T2U1 bos taurus
40	3	15.8	13	12 Q9WMC5	Q9WMC5 sigma virus
41	3	15.8	14	2 Q9R8P6	Q9R8P6 chlamydia t
42	3	15.8	14	2 Q9R8P2	Q9R8P2 chlamydia t
43	3	15.8	14	2 Q9R8N9	Q9R8N9 chlamydia t
44	3	15.8	14	2 Q9R8N6	Q9R8N6 chlamydia t
45	3	15.8	14	2 Q9R8N2	Q9R8N2 chlamydia t

ALIGNMENTS

RESULT 1

ID	Q920G5	PRELIMINARY:	PRT:	14 AA.
DC	Q920G5;	01-MAY-1999 (TREMBLrel. 10, Created)		
DT	01-MAY-1999 (TREMBLrel. 10, Last sequence update)			
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)			
DE	SHORTER Isoform of Interleukin 15 (Fragment).			
GN	IL15 OR INTERLEUKIN 15.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-BALBC;			
RA	Nishimura H.;			
RL	Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.			
RP	SEQUENCE FROM N.A.			
RC	STRATIN-BALBC;			
RX	MEDLINE=98211658; PubMed=9551932;			
RA	Nishimura H., Washizu J., Nakamura N., Enomoto A., Yoshikai Y.;			
RT	"Translational efficiency is up-regulated by alternative exon in murine IL-15 mRNA."			
RL	J. Immunol. 160:936-942(1998).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Prinz M., Hantsch U.R., Kettenmann H., Kirchhoff F.;			
RT	"Alternative splicing of mouse IL-15 is due to the use of an internal splice site in exon 5."			
RL	Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: A602307; BAA37122.1; -			
DR	EMBL: A012587; CAA10069.1; -			
DR	MGI:103014; 1115.			
FT	NON_TER			
SO	SEQUENCE			
	14 AA; 1503 MW; 62AA3C3889924E2B CRC64;			
	Query Match	26.3%;	Score 5;	DB 11; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSKEL 18
|||||
Db 4 SSKEL 8

RESULT 2

O16310 PRELIMINARY; PRT; 17 AA.
AC O16310;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-1999 (TREMBlrel. 09, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE GC*2 protein (Fragment).
GN GC*2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;

SEQUENCE FROM N.A.
[1]
RX MEDLINE=95242701; PubMed=7725672;
RA Kofler A., Braun A., Jenkins T., Serjeantson S.W., Cleve H.;
RT "Characterization of mutants of the vitamin-D-binding protein/group
specific component: GC aborigine (1A1) from Australian aborigines and
RT South African Blacks, and 2A9 from South Germany.";
RL Vox Sang. 68:50-54(1995).
DR EMBL: S77130; MADD14250.1; -.
FT NON_TER 17
SQ SEQUENCE 17 AA; 1845 MW; BB26CAD60293722C CRC64;

Query Match 21.1%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 KELA 19
|||||
Db 7 KELA 10

RESULT 3

O13376 PRELIMINARY; PRT; 17 AA.
AC O13376;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE RNA binding motif (Fragment).
GN RBM.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RN NCI
RP SEQUENCE FROM N.A.
RX MEDLINE=97032533; PubMed=8875892;
RA Prosser J., Inglis J.D., Conde A., Ma K., Kerr S., Thakrar R.,
RT Taylor K., Cameron J.K., Cooke H.J.;
RT "Degeneracy in human multicopy RBM (YRRM), a candidate spermatogenesis
gene.";
RL Mamm. Genome 7:835-842(1996).
DR EMBL: U38450; AAB49815.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2060 MW; 98CD6AEFE350012 CRC64;

Query Match 21.1%; Score 4; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
|||||

Db 3 GRGR 6

RESULT 4

O16271 PRELIMINARY; PRT; 19 AA.
ID O16271
AC O16271;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Arginine vasopressin V2 receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;

SEQUENCE FROM N.A.
[1]
RX MEDLINE=95086168; PubMed=7993996;
RA Holtzman E.J., Kolakowski L.F.Jr., Gelfman-Holtzman O., O'Brien D.G.,
RA Rasouipour M., Guillot A.P., Ausiello D.A.;
RT "Mutations in the vasopressin V2 receptor gene in two families with
RT nephrogenic diabetes insipidus.";
RL J. Am. Soc. Nephrol. 5:168-176(1994).
DR EMBL: S75754; AAB32753.1; -.
FT NON_TER 1
SQ SEQUENCE 19 AA; 1905 MW; 181640EFD90F2788 CRC64;

Query Match 21.1%; Score 4; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPGH 5
|||||
Db 1 VPGH 4

RESULT 5

O90U21 PRELIMINARY; PRT; 20 AA.
ID O90U21
AC O90U21;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Alpha class glutathione S-transferase subunit 2 (EC 2.5.1.18)
DE (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
[1]
RN NCI
RP SEQUENCE.
RX MEDLINE=96036981; PubMed=7485987;
RA Rouimi P., Debrauer L., Tulliez J.;
RT "Electrospray ionization-mass spectrometry as a tool for
RT characterization of glutathione S-transferase isozymes.";
RL Anal. Biochem. 229:304-312(1995).
SQ SEQUENCE 20 AA; 2412 MW; 9498D6E2C030B236 CRC64;

Query Match 21.1%; Score 4; DB 11; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
|||||
Db 11 GRGR 14

RESULT 6

P83067 PRELIMINARY; PRT; 10 AA.
ID P83067.
AC P83067;
DT 01-OCT-2001 (TREMBlrel. 18, Created)

DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
 DE 82 kDa protein (Fragment).
 OS Bacillus cereus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE, AND INDUCTION.
 RC STRAIN-NCIMB 11796;
 RA Browne N., Dowds B.C.A.;
 RL Submitted (Jun-2001) to the SWISS-PROT data bank.
 CC -1- INDUCTION: BY SALT STRESS.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1200 MW; 72DBA14B1325AAEB CRC64;

Query Match
 Best Local Similarity 15.8%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 SKE 17

DB 5 SKE 7

RESULT 7
 ID Q8RSU1 PRELIMINARY; PRT; 10 AA.
 AC Q8RSU1;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Urease alpha subunit (EC 3.5.1.5) (Fragment).
 OS UREA.
 GN Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1061;
 RA van Vliet A.H.M., Poppelaars S.W., Davies B.J., Scoof J.,
 RA Bereswill S., Kist M., Penn C.W., Kuipers E.J., Kuipers J.G.;
 RT "NMR mediates nickel-responsive transcriptional induction of urease
 RT expression in Helicobacter pylori.";
 RT Infect. Immun. 0:0-0(2002).
 DR EMBL: AY078177; AAL77213.1; -.
 KW Hydrolase.
 NON_TER 10 10
 SEQUENCE 10 AA; 1202 MW; 57C29E2B132771A7 CRC64;

Query Match
 Best Local Similarity 15.8%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KEL 18
DB 6 KEL 8

RESULT 8
 ID P82937 PRELIMINARY; PRT; 10 AA.
 AC P82937;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Unknown endospore protein B (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;

RN [1]
 RP SEQUENCE.
 RC STRAIN=CV. BOMI; TISSUE=STARCHY ENDOSPERM;
 RX MEDLINE=21088911; PubMed=11271488;
 RA Kristoffersen H.E., Flengsrud R.;
 RT "Separation and characterization of basic barley seed proteins.";
 RL Electrophoresis 21:3693-3700(2000).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 8.5-9.0, ITS MW IS: 11.9 KDA.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1297 MW; 8248A50B11PB5EBA CRC64;

Query Match
 Best Local Similarity 15.8%; Score 3; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HER 7

DB 6 HER 8

RESULT 9
 ID Q9QVE7 PRELIMINARY; PRT; 10 AA.
 AC Q9QVE7;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Beta 2-glycoprotein I, beta 2-GPI (Fragment).
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10118;
 RN [1]
 RP SEQUENCE.
 RA MEDLINE=92135065; PubMed=1777418;
 RX Matsura E., Igarashi M., Igarashi Y., Nagae H., Ichikawa K.,
 RA Yasuda T., Koike T.;
 RT "Molecular definition of human beta 2-glycoprotein I (beta 2-GPI) by
 RT alternation of anticardiolipin binding.";
 RT Int. Immunol. 3:1217-1221(1991).
 RL Int. Immunol. 3:1217-1221(1991).
 FT NON_TER 10 10
 SEQUENCE 10 AA; 1100 MW; 94E681B767376EA1 CRC64;

Query Match
 Best Local Similarity 15.8%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GRT 13
DB 1 GRT 3

RESULT 10
 ID Q9QVE8 PRELIMINARY; PRT; 10 AA.
 AC Q9QVE8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Protamine MP2 intermediate protein pM2/16 (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92174934; PubMed=1541289;
 RX Chauviere M., Martinge A., Debarie M., Sautiere P., Chevallier P.;
 RT "Molecular characterization of six intermediate proteins in the
 RT processing of mouse protamine p2 precursor.";

RL Eur. J. Biochem. 204:759-765(1992).
 FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1224 MW; DA050B040B11EAB6 CRC64;

Query Match 15.8%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 HER 7
 111
 DB 5 HER 7

RESULT 11
 O9QVE7 PRELIMINARY; PRT; 10 AA.
 AC O9QVE7;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 Protelime MP2 intermediate protein PMP2/20 (Fragment).

OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10095;

RN [1]
 RP MEDLINE=92174934; PubMed=1541289;
 RA Chauviere M., Martinage A., Debarle M., Sautiere P., Chevallier P.;
 RT "Molecular characterization of six intermediate proteins in the
 processing of mouse protelime P2 precursor."
 RL Eur. J. Biochem. 204:759-765(1992).

FT NON_TER 1
 FT NON_TER 10
 SQ SEQUENCE 10 AA; 1197 MW; 79920ED866DB1B04 CRC64;

Query Match 15.8%; Score 3; DB 11; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 HER 7
 111
 DB 1 HER 3

RESULT 12
 O9UR95 PRELIMINARY; PRT; 11 AA.
 O9UR95;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
 DE Heat shock protein 60 homolog (Fragment).
 OS Pichia angusta (Yeast) (Hansenula polymorpha).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Pichia.
 OX NCBI_TaxID=4905;

RN [1]
 RP MEDLINE=93223840; PubMed=8096822;
 RA Evers M.E., Hulse B., Tiltorenko V.I., Kunau W.H., Hartl F.U.,
 RA Harder W., Veenhuis M.;
 RT "Affinity purification of molecular chaperones of the yeast Hansenula
 polymorpha using immobilized denatured alcohol oxidase."
 RL FEBS Lett. 321:32-36(1993).

FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C372B CRC64;

Query Match 15.8%; Score 3; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 KEL 18

DB 111
 3 KEL 5

RESULT 13
 O60614 PRELIMINARY; PRT; 11 AA.
 AC O60614;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE MTG8 related protein (Fragment).

GN MTG8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=99009318; PubMed=9790752;
 RA Calabi F., Chilli V.;
 RT "CBFA2TL1, a gene rearranged in human Leukemia, is a member of a
 multigene family."
 RL Genomics 52:332-341(1998).

DR EMBL; AF052211; AAC64700.1;
 FT NON_TER 11
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1047 MW; CF001CE4DD86772 CRC64;

Query Match 15.8%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPG 4
 111
 DB 4 VPG 6

RESULT 14
 O9NV38 PRELIMINARY; PRT; 11 AA.
 ID O9NV38
 AC O9NV38;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
 DE Heavy metal-responsive transcription factor (Fragment).
 OS MTF-1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Auf der Maur A., Belser T., Wang Y., Gunes C., Lichtlen P.,
 RA Georgiev O., Schaffner W.;
 RT "Characterization of the mouse gene for the heavy metal-responsive
 transcription factor MTF-1."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ251881; CAB71327.1;
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1099 MW; A8653693773772C6 CRC64;

Query Match 15.8%; Score 3; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRG 11
 111
 DB 8 GRG 10

RESULT 15

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P83321
ID P83321 PRELIMINARY: PRT: 11 AA.
AC P83321;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FMRamide-like neuropeptide FLIP6 (DGRTPALRLRF-amide).
OS Peneaus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Peneaus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=EYESTALK;
RA Sithigorngul P., Pupnem J., Krungkarn C., Longyatt S.,
RA Chaivuthangkura P., Sithigorngul W., Pelsom A.;
RA "Seven novel FMRamide-like neuropeptide sequences from the eyestalk
of the giant tiger prawn Peneaus monodon."
Comp. Biochem. Physiol. 131B:325-337(2002).
RT -1- MASS SPECTROMETRY: MW=1301.8; METHOD=MALDI.
RT -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC NEUROPEPTIDE; Amidation.
KM MOD.RES 11 11 AMIDATION.
FT SEQUENCE 11 AA; 1301 MW; 9A19C860072DC771 CRC64;
SQ
Query Match 15.8%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
Db 2 GRT 4

RESULT 16
O9VN99 PRELIMINARY: PRT: 11 AA.
AC O9VN99;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE CG2676 protein.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Kocha S., Dunkov B.C., Dunn P.,
RA Duzin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fouts C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegwan C.,

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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
RA Palazzolo M., Pittman K.A., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svrlskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zavei J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
Science 287:2185-2195(2000).
RL EMBL: AE003603; AAF52049.1;
DR Flybase: FBgn0037309; CG2676.
SQ SEQUENCE 11 AA; 1113 MW; 8760FE9B05A1B1B1 CRC64;

Query Match 15.8%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSK 16
Db 9 SSK 11

RESULT 17
P82698 PRELIMINARY: PRT: 11 AA.
ID P82698;
AC P82698;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Periviscerokinin-1 (LEM-PVK-1).
OS Leucophaea maderae (Madaira cockroach).
OS Nauphoeta cinerea (Cinereous cockroach) (Gray cockroach),
OS Blaberus craniifer,
OS Blaptica dubia, and
OS Gromphadoria portentosa (Cockroach).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blaberoidea; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988, 6990, 6982, 132935, 36953;
RN [1]
RP SEQUENCE, FUNCTION, AND MASS SPECTROSCOPY.
RC TISSUE=ABDOMINAL PERISYMPHATIC ORGANS;
RX MEDLINE=20307624; PubMed=10849006;
RA Predel R., Kellner R., Baggerman G., Steilmetzer T., Schoofs L.;
RT "Identification of novel periviscerokinin from single neurohaemal
RT release sites in insects. MS/MS fragmentation complemented by Edman
RT degradation."
Eur. J. Biochem. 267:3869-3873(2000).
CC -1- FUNCTION: MEDIATES VISCERAL MUSCLE CONTRACTILE ACTIVITY
CC (MYOTROPIC ACTIVITY).
CC -1- MASS SPECTROMETRY: MW=1090.6; METHOD=MALDI.
KM NEUROPEPTIDE; Amidation.
FT MOD.RES 11 11 AMIDATION.
SQ SEQUENCE 11 AA; 1091 MW; 2C2D80E2D7605728 CRC64;

Query Match 15.8%; Score 3; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
Db 9 GRT 11

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RESULT 18
O9TRW5 PRELIMINARY: PRT: 11 AA.
ID 09TRW5
AC 09TRW5
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 25 kDa protein p25, peptide F4 (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=91372400; PubMed=1909972;
RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Omori A., Sato S.,
RA Shiratsuchi A., Uchida T., Imahori K.;
RA "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a
Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.",
PEPS Lett. 289:37-43(1991).
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 15.8%; Score 3; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRG 11
DB 8 GRG 10

RESULT 19
O04I31 PRELIMINARY: PRT: 11 AA.
ID 004I31
AC 004I31
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Wound induced protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-PIK-RED; TISSUE=PERICARP;
RA MEDLINE=91355936; PubMed=1715787;
RA Parsons B.L., Mattoo A.K.;
RA "Wound regulated accumulation of specific transcripts in tomato
fruit: interactions with fruit development, ethylene and light.",
RL Plant Mol. Biol. 17:453-464(1991).
DR EMBL: X59884; CAA42539.1;
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1278 MW; 92CB25782873325 CRC64;

Query Match 15.8%; Score 3; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSK 16
DB 3 SSK 5

RESULT 20
O99N81 PRELIMINARY: PRT: 11 AA.
ID 099N81
AC 099N81

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DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Delta like 1 (Fragment).
GN DLI1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Nakayama K.;
RA "Multiple POU-binding motifs, recognized by tissue-specific nuclear
factor(S), are important for Dll1 gene expression in developing neural
precursor cells.";
RT precursor cells";
RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AB050457; BAB43867.1;
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1259 MW; 33C3634CHDC40B07 CRC64;

Query Match 15.8%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 MGR 10
DB 1 MGR 3

RESULT 21
O92IH5 PRELIMINARY: PRT: 11 AA.
ID 092IH5
AC 092IH5
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Insulin receptor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94365199; PubMed=8083370;
RA Huang Z., Bodkin N.L., Ortmeier H.K., Hansen B.C., Shuldiner A.R.;
RA "Hyperinsulinemia is associated with altered insulin receptor mRNA
splicing in muscle of the spontaneously obese diabetic rhesus
monkey.";
RT monkey.";
RL J. Clin. Invest. 94:1289-1296(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Ying L.;
RA Submitted (JUN-1995) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Liu Y.;
RA Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RL EMBL: I42997; AAC96365.1;
DR EMBL: I42997; AAC96365.1;
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1052 MW; 9C25F7BAD8744865 CRC64;

Query Match 15.8%; Score 3; DB 11; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TSS 15
DB 2 TSS 4

RESULT 22

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089616
ID Q89616 PRELIMINARY; PRT; 11 AA.
AC Q89616;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE Hypothetical 1.2 kDa protein.
OS Avian infectious bronchitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirinae.
OX NCBI_TaxID=11120;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87111468; PubMed=3027249;
RA Boursnell M.E., Brown T.D.K., Foulds I.J., Green P.F., Tomley F.M.,
RA Bins M.M.;
RT "Completion of the sequence of the genome of the coronavirus avian
RT infectious bronchitis virus."
RT J. Gen. Virol. 68:57-77(1987).
[2]
SEQUENCE FROM N.A.
MEDLINE=88130171; PubMed=2829522;
RA Boursnell M.E., Brown T.D., Foulds I.J., Green P.F., Tomley F.M.,
RA Bins M.M.;
RT "The complete nucleotide sequence of avian infectious bronchitis
RT virus: analysis of the polymerase-coding region."
RT Adv. Exp. Med. Biol. 218:15-29(1987).
DR EMBL; M64355; AAA46322.1; -.
DR EMBL; M27471; AAA85340.1; -.
KM Hypothetical protein.
SQ SEQUENCE 11 AA; 1182 MW; 251EE3F165B721E8 CRC64;

Query Match 15.8%; Score 3; DB 12; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PGH 5
DB 3 PGH 5

RESULT 23
09D232 PRELIMINARY; PRT; 11 AA.
ID Q9D232;
AC Q9D232;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE Gag polyprotein (Fragment).
OS Human immunodeficiency virus type 1.
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20461476; PubMed=11005867;
RA Martinez-Picado J., Depasquale M.P., Kartsonis N., Hanna G.J.,
RA Wong J., Pinzi D., Rosenberg F., Gunthard H.F., Sutton L., Savara A.,
RA Petropoulos C.J., Hellmann N., Walker B.D., Richman D.D.,
RA Siliciano R., D'Aquila R.T.;
RT "Antiretroviral resistance during successful therapy of HIV type 1
RT infection."
RT Proc. Natl. Acad. Sci. U.S.A. 97:10948-10953(2000).
DR EMBL; AF292799; AAG25407.1; -.
KM Polyprotein.
FT NON-TER 1
SQ SEQUENCE 11 AA; 1386 MW; 79DC73C0145771B4 CRC64;

Query Match 15.8%; Score 3; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GRT 13

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DB 3 GRT 5

RESULT 24
09K7A4 PRELIMINARY; PRT; 11 AA.
ID Q9K7A4;
AC Q9K7A4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE Hypothetical protein BH3464.
OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C-125 / JCM 9153;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.;
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis."
RT Nucleic Acids Res. 28:4317-4331(2000).
DR EMBL; AP001518; BA807183.1; -.
KM Hypothetical protein; Complete proteome.
SQ SEQUENCE 11 AA; 1219 MW; 5F7D23CB727B13 CRC64;

Query Match 15.8%; Score 3; DB 16; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KEL 18
DB 4 KEL 6

RESULT 25
050303 PRELIMINARY; PRT; 12 AA.
ID Q50303;
AC Q50303;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DE Hypothetical 1.4 kDa protein (Fragment).
OS Bacillus stearothermophilus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Geobacillus.
OX NCBI_TaxID=1422;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CCM 2184;
RA Vlasova H., Krasny L., Rucik V., Jonak J.;
RT "The pyrad gene coding for the large subunit of Carboxylphosphate
RT synthetase from Bacillus stearothermophilus: Molecular cloning and
RT functional characterization."
RT Folia Biol. (Praha) 44:163-172(1998).
DR EMBL; AJ001805; CAA05021.1; -.
KM Hypothetical protein.
FT NON-TER 12
SQ SEQUENCE 12 AA; 1379 MW; 70087CB0E8A6840B CRC64;

Query Match 15.8%; Score 3; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERM 8
DB 5 ERM 7

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Mon May 12 15:26:59 2003

us-09-674-913a-1.oligo.rspt

Page 8

Search completed: May 9, 2003, 16:07:38
Job time : 86 secs

GenCore version 5.1.4-p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 16:04:59 ; Search time 29 Seconds
(Without alignments)
19.277 Million cell updates/sec

Title: US-09-674-913a-1

Perfect score: 19

Sequence: 1 NPGHERMGRGRSSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 262574 seqs, 29422922 residues

size: 0
Total number of hits satisfying chosen parameters: 66571

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database: Issued_Patents_AA:*
1: /cgn2_6/prodata1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata1/1aa/5C_COMB.pep:*
4: /cgn2_6/prodata1/1aa/5D_COMB.pep:*
5: /cgn2_6/prodata1/1aa/5E_COMB.pep:*
6: /cgn2_6/prodata1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	10	52.6	10	US-08-726-306A-1	Sequence 1, Appl
2	4	21.1	10	US-08-482-228-202	Sequence 202, App
3	4	21.1	10	US-08-310-912A-95	Sequence 95, Appl
4	4	21.1	10	US-09-139-762A-39	Sequence 39, Appl
5	4	21.1	10	US-09-139-762A-102	Sequence 102, App
6	4	21.1	10	US-08-482-528-202	Sequence 202, App
7	4	21.1	10	US-08-159-339A-669	Sequence 669, App
8	4	21.1	10	US-08-841-089-95	Sequence 95, Appl
9	4	21.1	10	US-09-301-085-95	Sequence 95, Appl
10	4	21.1	10	US-09-479-431A-5	Sequence 5, Appl
11	4	21.1	10	PCT-US95-04570-95	Sequence 95, Appl
12	4	21.1	10	PCT-US95-04589-95	Sequence 95, Appl
13	4	21.1	10	5210075-7	Patent No. 5210075
14	4	21.1	11	US-08-960-128-5	Sequence 5, Appl
15	4	21.1	11	US-08-350-260A-484	Sequence 484, Appl
16	4	21.1	11	US-08-642-246-35	Sequence 35, Appl
17	4	21.1	11	US-09-133-062D-26	Sequence 26, Appl
18	4	21.1	11	US-09-297-981-18	Sequence 18, Appl
19	4	21.1	11	US-09-451-206-35	Sequence 35, Appl
20	4	21.1	11	PCT-US96-06229-35	Sequence 35, Appl
21	4	21.1	12	US-08-548-540-155	Sequence 155, App
22	4	21.1	12	US-08-687-590-5	Sequence 5, Appl
23	4	21.1	12	US-09-461-697-439	Sequence 439, Appl
24	4	21.1	12	US-09-297-981-30	Sequence 30, Appl
25	4	21.1	12	US-07-946-180B-13	Sequence 13, Appl
26	4	21.1	12	PCT-US96-09809-155	Sequence 155, App
27	4	21.1	13	US-08-452-722-1	Sequence 1, Appl

28	4	21.1	13	US-08-404-731A-1	Sequence 1, Appl
29	4	21.1	13	US-08-344-227-1	Sequence 1, Appl
30	4	21.1	13	US-08-503-226B-1	Sequence 1, Appl
31	4	21.1	13	US-08-834-314-5	Sequence 5, Appl
32	4	21.1	13	US-08-721-458B-1	Sequence 1, Appl
33	4	21.1	13	US-08-444-818-129	Sequence 129, App
34	4	21.1	13	US-09-155-941-14	Sequence 14, App
35	4	21.1	13	US-09-155-941-18	Sequence 18, App
36	4	21.1	13	US-09-155-941-22	Sequence 22, App
37	4	21.1	13	PCT-US94-10257A-50	Sequence 29, App
38	4	21.1	14	US-08-321-668-29	Sequence 29, App
39	4	21.1	14	US-08-837-941-29	Sequence 29, App
40	4	21.1	14	US-08-651-818A-20	Sequence 20, App
41	4	21.1	14	US-08-722-806A-10	Sequence 10, App
42	4	21.1	14	US-09-184-826-20	Sequence 20, App
43	4	21.1	14	US-09-337-028-10	Sequence 10, App
44	4	21.1	14	US-09-597-877-10	Sequence 10, App
45	4	21.1	14	PCT-US93-06751-62	Sequence 62, App

ALIGNMENTS

RESULT 1
US-08-726-306A-1
Sequence 1, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henr
APPLICANT: Grosveld, Franklin G.
TITLE OF INVENTION: DIAGNOSIS METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,306A
FILING DATE: 02-Oct-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: GB 95/20080.4
FILING DATE: 02-Oct-1995
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 60/009,832
FILING DATE: 01-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph.D., Kathleen M.
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 96,048-A (3255/00784)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 345-9100
TELEFAX: (617) 345-9111
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-726-306A-1
Query Match 52.6%, Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00017;
Matches 10; Conservative 0; Mismatches 0; Indels 0;

QY 10 RGRSSKELA 19
 |||||
 Db 1 RGRSSKELA 10

RESULT 2
 US-08-482-228-202
 ; Sequence 202, Application US/08482228

Patent No. 5968753
 GENERAL INFORMATION:
 APPLICANT: Tseng-Law, Janet
 APPLICANT: Kabori, Joan A.
 APPLICANT: Al-Abdaly, Fahad A.
 APPLICANT: Guillemo, Roy
 APPLICANT: Helgeson, Sam L.
 APPLICANT: Deans, Robert J.
 TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
 TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
 NUMBER OF SEQUENCES: 215
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Janice Guthrie, Ph.D.
 STREET: P.O. Box 15210
 CITY: Irvine
 STATE: California
 COUNTRY: USA
 ZIP: 92713-5210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,228
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Guthrie, Janice
 REGISTRATION NUMBER: 35,170
 REFERENCE/DOCKET NUMBER: IT-4630CIP3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (714) 440-5353
 TELEFAX: (714) 553-1952
 INFORMATION FOR SEQ ID NO: 202:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-482-228-202

Query Match 21.1%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TSSK 16
 ||||
 Db 6 TSSK 9

RESULT 3
 US-08-310-912A-95
 ; Sequence 95, Application US/08310912A
 Patent No. 5981730

GENERAL INFORMATION:
 APPLICANT: Ausubel, Frederick M.
 APPLICANT: Staskawicz, Brian J.
 APPLICANT: Brent, Andrew F.
 APPLICANT: Dahlbeck, Douglas
 APPLICANT: Katagiri, Fumitaki
 APPLICANT: Kunkel, Barbara N.
 APPLICANT: Mindrinos, Michael N.
 APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND DETECTION
 TITLE OF INVENTION: METHODS
 NUMBER OF SEQUENCES: 208
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2904

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/310,912A
 FILING DATE: September 22, 1994
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/227,360
 FILING DATE: April 13, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Lech, Karen F.
 REGISTRATION NUMBER: 35,238
 REFERENCE/DOCKET NUMBER: 00786/254001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 100234
 INFORMATION FOR SEQ ID NO: 95:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-310-912A-95

Query Match 21.1%; Score 4; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPGH 5
 ||||
 Db 3 VPGH 6

RESULT 4
 US-09-139-762A-39
 ; Sequence 39, Application US/09139762A
 Patent No. 6013453

GENERAL INFORMATION:
 APPLICANT: Choo, Yen
 APPLICANT: Klug, Aaron
 APPLICANT: Sanchez Garcia, Isidro
 TITLE OF INVENTION: Improvements in or Relating to
 TITLE OF INVENTION: Binding Proteins for Recognition of DNA
 NUMBER OF SEQUENCES: 125
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/139,762A

FILED DATE: 20-AUG-1994
CLASSIFICATION: 102
PRIORITY APPLICATION NUMBER: US 08/793,408
APPLICATION NUMBER: 02-JUN-1997
PRIORITY APPLICATION NUMBER: PCT/GB95/01949
FILED DATE: 17-AUG-1995
PRIORITY APPLICATION NUMBER: GB 9514698.1
APPLICATION NUMBER: 18-JUL-1995
PRIORITY APPLICATION DATA: GB 9422534.9
FILED DATE: 08-NOV-1994
PRIORITY APPLICATION DATA: GB 9416880.4
APPLICATION NUMBER: 20-AUG-1994
FILED DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 39
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-39

Query Match 21.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GHER 7
DB 7 GHER 10

RESULT 5
US-09-139-762A-102
Sequence 102, Application US/09139762A
Patent No. 6013453
GENERAL INFORMATION:
APPLICANT: Choo, Yen
APPLICANT: King, Aaron
APPLICANT: Sanchez Garcia, Isidro
TITLE OF INVENTION: Improvements in or Relating to
TITLE OF INVENTION: Binding Proteins for Recognition of DNA
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESS: Pillsbury Madison & Sutro, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/139,762A
FILED DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/793,408
FILED DATE: 02-JUN-1997
PRIORITY APPLICATION DATA: PCT/GB95/01949
APPLICATION NUMBER: 17-AUG-1995
FILED DATE: 17-AUG-1995
PRIORITY APPLICATION DATA: GB 9514698.1
APPLICATION NUMBER: 18-JUL-1995
FILED DATE: 18-JUL-1995
PRIORITY APPLICATION DATA: GB 9422534.9
APPLICATION NUMBER: 08-NOV-1994
FILED DATE: 08-NOV-1994
PRIORITY APPLICATION DATA:

APPLICATION NUMBER: GB 9416880.4
FILED DATE: 20-AUG-1994
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-139-762A-102

Query Match 21.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GHER 7
DB 7 GHER 10

RESULT 6
US-08-482-528-202
Sequence 202, Application US/08482528
Patent No. 6017719
GENERAL INFORMATION:
APPLICANT: Tseng-Law, Janet
APPLICANT: Kobori, Joan A.
APPLICANT: Al-Abdaly, Fahad A.
APPLICANT: Guillermo, Roy
APPLICANT: Helgeson, Sam L.
APPLICANT: Deans, Robert J.
TITLE OF INVENTION: POSITIVE AND NEGATIVE CELL
TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
NUMBER OF SEQUENCES: 215
CORRESPONDENCE ADDRESS:
ADDRESS: Janice Guthrie, Ph.D.
STREET: P.O. Box 15210
CITY: Irvine
STATE: California
COUNTRY: USA
ZIP: 92713-5210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,528
FILED DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Guthrie, Janice
REGISTRATION NUMBER: 35,170
REFERENCE/DOCKET NUMBER: IT-4630C1P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (714) 440-5353
TELEFAX: (714) 553-1952
INFORMATION FOR SEQ ID NO: 202:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-482-528-202

Query Match 21.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TSSK 16
DB 6 TSSK 9

RESULT 7
US-08-159-339A-669
; Sequence 669, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 669:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-669
Query Match 21.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 MGRG 11
|||||
Db 5 MGRG 8

RESULT 8
US-08-841-089-95
; Sequence 95, Application US/08841089
; Patent No. 6127607
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.

APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street Suite 3100
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2904
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.308
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/841,089
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/227,360
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00786/230001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 100254
; INFORMATION FOR SEQ ID NO: 95:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-841-089-95
Query Match 21.1%; Score 4; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPCH 5
|||||
Db 3 VPCH 6

RESULT 9
US-09-301-085-95
; Sequence 95, Application US/09301085
; Patent No. 6262248
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/301,085
; EARLIER FILING DATE: 1999-04-28
; EARLIER APPLICATION NUMBER: 08/310,912
; EARLIER FILING DATE: 1994-09-22
; EARLIER APPLICATION NUMBER: 08/227,360
; EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 95
LENGTH: 10
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-09-301-085-95

Query Match 21.1%: Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPGH 5
1111
DB 3 VPGH 6

RESULT 10
US-09-479-431A-5
Sequence 5, Application US/09479431A
Patent No. 6413556
GENERAL INFORMATION:

APPLICANT: Sky High, LLC
APPLICANT: Bathurst, Ian C.

APPLICANT: Foeht, Matthew
TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
FILE REFERENCE: 4147-23

CURRENT APPLICATION NUMBER: US/09/479,431A
CURRENT FILING DATE: 2002-03-12

NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1

SEQ ID NO 5
LENGTH: 10
TYPE: PRT

ORGANISM: Glycine max
FEATURE:

NAME/KEY: misc.feature
LOCATION: (1)..(10)

OTHER INFORMATION: Xaa = any amino acid
US-09-479-431A-5

Query Match 21.1%: Score 4; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TSSK 16
1111
DB 2 TSSK 5

RESULT 11
US95-04570-95
Sequence 95, Application PC/TUS9504570
GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.

APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas

APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.

APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street Suite 3100
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110-2904
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04570

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360

FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

TELEX: 100254
INFORMATION FOR SEQ ID NO: 95:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids

TYPE: amino acid
STRANDEDNESS: not relevant

TOPOLOGY: linear
MOLECULE TYPE: protein

PCT-US95-04570-95

Query Match 21.1%: Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPGH 5
1111
DB 3 VPGH 6

RESULT 12
PCT-US95-04589-95
Sequence 95, Application PC/TUS9504589
GENERAL INFORMATION:

APPLICANT: Ausubel, Frederick M.
APPLICANT: Staskawicz, Brian J.

APPLICANT: Brent, Andrew F.
APPLICANT: Dahlbeck, Douglas

APPLICANT: Katagiri, Fumiaki
APPLICANT: Kunkel, Barbara N.

APPLICANT: Mindinos, Michael N.
APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: RPS2 GENE AND USES THEREOF
NUMBER OF SEQUENCES: 201

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street Suite 3100
CITY: Boston

STATE: MA
COUNTRY: USA

ZIP: 02110-2904
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04589

FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/227,360

FILING DATE: 13-APR-1994
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00786/230001
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 100254
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04589-95

Query Match 21.1%; Score 4; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPGH 5
Db 3 VPGH 6

Patent No. 5210075
GOBI:LOBL THOMAS J.
TITLE OF INVENTION: INTERLEUKIN 6 ANTAGONIST PEPTIDES
NUMBER OF SEQUENCES: 69
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,868
FILING DATE: 16-FEB-1990
SEQ ID NO: 7;
LENGTH: 10

Query Match 21.1%; Score 4; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SSKK 17
Db 2 SSKK 5

RESULT 14
US-08-960-128-5
Sequence 5, Application US/08960128
Patent No. 5951985

GENERAL INFORMATION:

APPLICANT: Butler, Sandra M.
APPLICANT: Pomato, Nicholas
APPLICANT: Bos, Ebo
APPLICANT: Hanna, Michael G.
APPLICANT: Haspel, Martin V.
APPLICANT: Hoover, Herbert C.
TITLE OF INVENTION: Tumor Associated Epitopes
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5951985el Patent Department
STREET: 1300 Piccard Drive, Suite 206
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/960,128
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/478,591

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Gormley, Mary E.

REGISTRATION NUMBER: 34,409

TELECOMMUNICATION INFORMATION:

TELEPHONE: (301) 258-5200

TELEFAX: (301) 977-0847

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

HYPOTHETICAL: NO

US-08-960-128-5

Query Match 21.1%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
Db 1 RTSS 4

RESULT 15
US-08-350-260A-484

Sequence 484, Application US/08350260A

Patent No. 5962255

GENERAL INFORMATION:

APPLICANT: Winter, Gregory Paul
APPLICANT: Griffiths, Andrew David
APPLICANT: Williams, Samuel Cameron
APPLICANT: Waterhouse, Peter
APPLICANT: Missim, Ahuya
APPLICANT: Johnson, Kevin Stuart
APPLICANT: Smith, Andrew John Hammond
TITLE OF INVENTION: Methods for producing members of specific
NUMBER OF SEQUENCES: 602
CORRESPONDENCE ADDRESS:
ADDRESSEE: David W. Clough
STREET: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/350,260A
FILING DATE: 05-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9110549.4
FILING DATE: 15-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9206318.9
FILING DATE: 24-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB91/01134
FILING DATE: 10-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB92/00883
FILING DATE: 15-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00605

FILING DATE: 24-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/150,002
FILING DATE: 31-MAR-1994
PRIOR APPLICATION DATA: US 08/307,619
APPLICATION NUMBER: US 08/307,619
FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 28111/32372
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
INFORMATION FOR SEQ ID NO: 484:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-350-260A-484

Query Match 21.1%; Score 4; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
DB 1 GRGR 4

RESULT 16
US-08-642-246-35
Sequence 35, Application US/08642246

Patent No. 6033654
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Erwin R.
APPLICANT: CAPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
TITLE OF INVENTION: Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,246
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Berttram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-246-35

Query Match 21.1%; Score 4; DB 3; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
DB 2 GRGR 5

RESULT 17
US-09-133-062D-26
Sequence 26, Application US/09133062D
Patent No. 6258776
GENERAL INFORMATION:
APPLICANT: Hemmings, Brian A
APPLICANT: Millward, Thomas A
TITLE OF INVENTION: Calcium Regulated Kinase
FILE REFERENCE: 30110
CURRENT APPLICATION NUMBER: US/09/133,062D
CURRENT FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: GB 9717089.8
PRIOR FILING DATE: 1997-08-12
PRIOR APPLICATION NUMBER: GB 9717499.9
PRIOR FILING DATE: 1998-08-19
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide
US-09-133-062D-26

Query Match 21.1%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
DB 4 RTSS 7

RESULT 18
US-09-297-981-18
Sequence 18, Application US/09297981
Patent No. 6362007
GENERAL INFORMATION:
APPLICANT: MEHENS, LYDIE
APPLICANT: LOHRMANN, REINHARD GEORGE
APPLICANT: UNION, ANN
APPLICANT: RAYMAKERS, JOSEPH
TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE
TITLE OF INVENTION: ANTIBODIES FROM SERA OF LIVING BEINGS AFFECTED WITH
TITLE OF INVENTION: SYSTEMIC LUPUS ERYTHEMATOSUS
FILE REFERENCE: INNS011-
CURRENT APPLICATION NUMBER: US/09/297,981
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-297-981-18

Query Match 21.1%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12

DB 3 GRGR 6

RESULT 19

US-09-451-206-35
Sequence 35, Application US/09451206
Patent No. 6423333
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Edwin R.
CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/451,206
FILING DATE: 29-NOV-6423333-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,246
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 35:
9-451-206-35

Query Match 21.1%; Score 4; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
DB 2 GRGR 5

RESULT 20
PCT-US96-06229-35
Sequence 35, Application PC/TUS9606229
GENERAL INFORMATION:
APPLICANT: STEDRONSKY, Edwin R.
CAPPELLO, Joseph
TITLE OF INVENTION: Tissue Adhesive Using Synthetic
Crosslinking
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: Four Embarcadero Center, Suite 200
CITY: San Francisco
STATE: CA

COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/06229
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A61127-1/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US96-06229-35

Query Match 21.1%; Score 4; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
DB 2 GRGR 5

RESULT 21
US-08-548-540-155
Sequence 155, Application US/08548540
Patent No. 5733731
GENERAL INFORMATION:
APPLICANT: Schatz, Peter J.
APPLICANT: Cull, Millard G.
APPLICANT: Miller, Jeff F.
APPLICANT: Stemmer, Willem P.C.
TITLE OF INVENTION: Peptide Library and Screening Method
NUMBER OF SEQUENCES: 162
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/548,540
FILING DATE: 26-OCT-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/290,641
FILING DATE: 15-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/963,321
FILING DATE: 15-OCT-1992
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 16528J-001240US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 155:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-548-540-155

Query Match
Best Local Similarity 21.1%; Score 4; DB 1; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GRGR 10
DB 4 GRGR 7

RESULT 22
US-08-687-590-5
Sequence 5, Application US/08687590
Patent No. 6255070
GENERAL INFORMATION:
APPLICANT: Willison, Keith Robert
APPLICANT: Kubota, Hiroshi
APPLICANT: Ashworth, Alan
TITLE OF INVENTION: Folding Proteins
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,590
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00192
FILING DATE: 31-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9401791.0
FILING DATE: 31-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9418234.2
FILING DATE: 09-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 084619-000000US
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-687-590-5

Query Match
Best Local Similarity 21.1%; Score 4; DB 4; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
DB 3 GRGR 6

RESULT 23
US-09-461-697-439
Sequence 439, Application US/09461697
Patent No. 6277974
GENERAL INFORMATION:
APPLICANT: COGENT NEUROSCIENCE, Inc.
APPLICANT: Lo, Donald C.
APPLICANT: Baimey, Shawn
APPLICANT: Thomas, Mary Beth
APPLICANT: Portbury, Stuart D.
APPLICANT: Puranam, Kasturi
APPLICANT: Katz, Lawrence C.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
FILE REFERENCE: 10001-005-999
CURRENT APPLICATION NUMBER: US/09/461,697
CURRENT FILING DATE: 1999-12-14
NUMBER OF SEQ ID NOS: 466
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 439
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-09-461-697-439

Query Match
Best Local Similarity 21.1%; Score 4; DB 4; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SSKE 17
DB 9 SSKE 12

RESULT 24
US-09-297-981-30
Sequence 30, Application US/09297981
Patent No. 6362007
GENERAL INFORMATION:
APPLICANT: MEHENS, LYDIE
APPLICANT: LUHRMANN, REINHARD GEORGE
APPLICANT: UNION, ANN
APPLICANT: RAYMAKERS, JOSEPH
TITLE OF INVENTION: METHYLATED, SMD HOMOLOGOUS PEPTIDES, REACTIVE WITH THE
TITLE OF INVENTION: ANTIBODIES FROM SERA OF LIVING BEINGS AFFECTED WITH
FILE REFERENCE: INNS011-
CURRENT APPLICATION NUMBER: US/09/297,981
CURRENT FILING DATE: 1999-05-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-297-981-30

Query Match
Best Local Similarity 21.1%; Score 4; DB 4; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
DB 5 GRGR 8

RESULT 25
US-07-946-180B-13

Sequence 13, Application US/07946180B
Patent No. 6369203

GENERAL INFORMATION:

APPLICANT: Zeppezauer, Michael

APPLICANT: Sch nberger, Arno

APPLICANT: Cebecauer, Ladislav

TITLE OF INVENTION: Peptides For The Production Of

TITLE OF INVENTION: Preparations For The Diagnosis

TITLE OF INVENTION: and Therapy Of Systemic Lupus

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Roseman & Collin

STREET: 575 Madison Avenue

CITY: New York

STATE: NY

COUNTRY: U.S.A.

ZIP: 10022-2585

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5"

COMPUTER: IBM PS2-286

OPERATING SYSTEM: MS-DOS

SOFTWARE: Wordperfect 5.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/946,180B

FILING DATE: 19920916

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 41 30 786.0

FILING DATE: 09/16/91

ATTORNEY/AGENT INFORMATION:

NAME: Weintraub, Bruce S.

REGISTRATION NUMBER: 34,277

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 940-8800

TELEFAX: (212) 940-8776/935-0679

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 AMINO ACIDS

TYPE: AMINO ACID

TOPOLOGY: LINEAR

MOLECULE TYPE: PEPTIDE

FRAGMENT TYPE: C-terminal fragment

ORIGINAL SOURCE:

ORGANISM: CALF

TISSUE TYPE: THYMUS

IMMEDIATE SOURCE: SYNTHETIC

FEATURE:

NAME/KEY: Peptide fragment

NAME/KEY: 114-125 derived

NAME/KEY: from histone H2B

LOCATION: Location 1 through 12 below

LOCATION: represents locations 114-125

LOCATION: in the published sequence.

IDENTIFICATION METHOD: By experiment

PUBLICATION INFORMATION:

AUTHORS: IWAI, K; et al;

TITLE:

JOURNAL: J. Biochem.

VOLUME: 72

PAGES: 357-367

DATE: 1972

US-07-946-180B-13

Query Match

Best Local Similarity 21.1%; Score 4; DB 4; Length 12;

Db 9 TSSK 12
Search completed: May 9, 2003, 16:08:14
Job time : 31 secs

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2003, 16:06:15 ; Search time 50 Seconds
(without alignments)
34.970 Million cell updates/sec

Title: US-09-674-913A-1

Perfect score: 19
Sequence: 1 NVPGHERMGRTSSKELA 19

Scoring table:
Gapop 60.0, Gapext 60.0

Searched: 349150 seqs, 92025710 residues

I size: 0

Total number of hits satisfying chosen parameters: 33076

Minimum DB seq length: 10

Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database: Published Applications_AA:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5	26.3	18	9	US-10-270-877-33	Sequence 33, App1
2	5	26.3	18	9	US-10-270-877-33	Sequence 33, App1
3	5	26.3	19	9	US-10-117-846-33	Sequence 33, App1
4	4	21.1	10	9	US-10-040-572-5	Sequence 5, App1
5	4	21.1	10	9	US-09-185-908-119	Sequence 119, App
6	4	21.1	10	9	US-09-185-908-128	Sequence 128, App
7	4	21.1	10	9	US-09-185-908-137	Sequence 137, App
8	4	21.1	10	9	US-09-185-908-146	Sequence 146, App
9	4	21.1	10	9	US-09-185-908-155	Sequence 155, App
10	4	21.1	10	9	US-09-899-046-219	Sequence 219, App
11	4	21.1	10	9	US-09-899-046-220	Sequence 220, App
12	4	21.1	10	9	US-09-899-046-221	Sequence 221, App
13	4	21.1	10	9	US-09-878-281-219	Sequence 219, App
14	4	21.1	10	9	US-09-878-281-220	Sequence 220, App
15	4	21.1	10	9	US-09-878-281-221	Sequence 221, App
16	4	21.1	10	9	US-09-572-404B-668	Sequence 668, App
17	4	21.1	10	9	US-09-572-404B-670	Sequence 670, App
18	4	21.1	10	9	US-09-572-404B-672	Sequence 672, App
19	4	21.1	10	9	US-09-572-404B-1028	Sequence 1028, App

20	4	21.1	10	9	US-09-572-404B-1300	Sequence 1300, Ap
21	4	21.1	10	9	US-09-572-404B-1302	Sequence 1302, Ap
22	4	21.1	10	9	US-09-572-404B-1368	Sequence 1368, Ap
23	4	21.1	10	9	US-09-572-404B-1484	Sequence 1484, Ap
24	4	21.1	10	9	US-09-572-404B-1576	Sequence 1576, Ap
25	4	21.1	10	9	US-09-572-404B-1580	Sequence 1580, Ap
26	4	21.1	10	9	US-09-572-404B-1582	Sequence 1582, Ap
27	4	21.1	10	9	US-09-572-404B-1720	Sequence 1720, Ap
28	4	21.1	10	9	US-09-572-404B-1722	Sequence 1722, Ap
29	4	21.1	10	9	US-09-572-404B-1732	Sequence 1732, Ap
30	4	21.1	10	9	US-09-572-404B-1784	Sequence 1784, Ap
31	4	21.1	10	9	US-09-572-404B-1843	Sequence 1843, Ap
32	4	21.1	10	9	US-09-572-404B-1845	Sequence 1845, Ap
33	4	21.1	10	9	US-09-572-404B-1847	Sequence 1847, Ap
34	4	21.1	10	9	US-09-572-404B-1849	Sequence 1849, Ap
35	4	21.1	10	9	US-09-572-404B-1851	Sequence 1851, Ap
36	4	21.1	10	9	US-09-572-404B-1853	Sequence 1853, Ap
37	4	21.1	10	9	US-09-572-404B-1855	Sequence 1855, Ap
38	4	21.1	10	9	US-09-572-404B-1857	Sequence 1857, Ap
39	4	21.1	10	9	US-09-572-404B-1859	Sequence 1859, Ap
40	4	21.1	10	9	US-09-572-404B-1861	Sequence 1861, Ap
41	4	21.1	10	9	US-09-572-404B-1863	Sequence 1863, Ap
42	4	21.1	10	9	US-09-572-404B-1865	Sequence 1865, Ap
43	4	21.1	10	9	US-09-572-404B-1867	Sequence 1867, Ap
44	4	21.1	10	9	US-09-572-404B-1869	Sequence 1869, Ap
45	4	21.1	10	9	US-09-572-404B-1871	Sequence 1871, Ap

ALIGNMENTS

RESULT 1
US-10-270-877-33
Sequence 33, Application US/10270877
Publication No. US20030049791A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD1
CURRENT APPLICATION NUMBER: US/10/270, 877
CURRENT FILING DATE: 2002-10-11
PRIOR APPLICATION NUMBER: 09/512, 563
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/121, 483
PRIOR FILING DATE: 1999-02-24
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 33
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Hypothetical
US-10-270-877-33
Query Match
Best Local Similarity 100.0%; Pred No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GRTSS 15
Db 14 GRTSS 18
RESULT 2
US-10-270-837-33
Sequence 33, Application US/10270837
Publication No. US20030054488A1
GENERAL INFORMATION:
APPLICANT: Saus, Juan
TITLE OF INVENTION: Goodpasture Binding Protein
FILE REFERENCE: 98-723-AD2

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; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 33
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hypothetical
; OTHER INFORMATION: peptide
US-10-270-837-33

Query Match
Best Local Similarity 100.0%; Score 5; DB 9; Length 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 GRTSS 15
14 GRTSS 18

RESULT 3
US-10-117-846-33
; Sequence 33, Application US/10117846
; Patent No. US20020168673A1
; GENERAL INFORMATION:
; APPLICANT: Fuller, Margaret T
; APPLICANT: Hales, Karen G.
; APPLICANT: Santel, Ansgar H.
; TITLE OF INVENTION: Mitofusins, Fzo Homologs and Functional
; FILE REFERENCE: STAN-063CIP3
; CURRENT APPLICATION NUMBER: US/10/117,846
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/413,285
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: PCT/US00/27871
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus
US-10-117-846-33

Query Match
Best Local Similarity 100.0%; Score 5; DB 9; Length 19;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 GRTSS 15
7 GRTSS 11

RESULT 4
US-10-040-572-5
; Sequence 5, Application US/10040572
; Patent No. US2002015183A1
; GENERAL INFORMATION:
; APPLICANT: Sky High, LLC
; APPLICANT: Bathurst, Ian C.
; APPLICANT: Foeht, Matthew
; TITLE OF INVENTION: AQUEOUS ANTI-APOPTOTIC COMPOSITIONS
; FILE REFERENCE: 4147-23-1
; CURRENT APPLICATION NUMBER: US/10/040,572
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; CURRENT FILING DATE: 2002-03-12
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: xaa = any amino acid
US-10-040-572-5

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

13 TSSK 16
2 TSSK 5

RESULT 5
US-09-185-908-119
; Sequence 119, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Gour, Barbara J.
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 119
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-119

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

12 RTSS 15
3 RTSS 6

RESULT 6
US-09-185-908-128
; Sequence 128, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; APPLICANT: Gour, Barbara J.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 128
; LENGTH: 10
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; FEATURE:
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-128

Query Match
  21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
   |||
   3 RTSS 6

RESULT 7
US-09-185-908-137
; Sequence 137, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 137
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-137

Query Match
  21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
   |||
   3 RTSS 6

RESULT 8
US-09-185-908-146
; Sequence 146, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 146
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
```

```
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-146

Query Match
  21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
   |||
   3 RTSS 6

RESULT 9
US-09-185-908-155
; Sequence 155, Application US/09185908A
; Publication No. US20020193294A1
; GENERAL INFORMATION:
; APPLICANT: Blaschuk, Orest W.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING CLAUDIN-MEDIATED
; FILE REFERENCE: 100086.409
; CURRENT APPLICATION NUMBER: US/09/185,908A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Product of
; OTHER INFORMATION: synthesis based on mouse claudin-2 sequence
; FEATURE:
; OTHER INFORMATION: Cyclic Peptide
US-09-185-908-155

Query Match
  21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 RTSS 15
   |||
   3 RTSS 6

RESULT 10
US-09-699-046-219
; Sequence 219, Application US/09899046
; Publication No. US2003008274A1
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: New sequences of hepatitis C virus
; TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
; NUMBER OF SEQUENCES: 270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/899,046
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/362,455
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

US-09-899-046-219

Query Match 21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRTS 14
||||
Db 4 GRTS 7

RESULT 11

US-09-899-046-220
; Sequence 220, Application US/09899046
; Publication No. US2003008274A1
; GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: New sequences of hepatitis C virus
TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,046

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362,455

FILING DATE:

INFORMATION FOR SEQ ID NO: 220:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-899-046-220

Query Match 21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRTS 14
||||
Db 4 GRTS 7

RESULT 12

US-09-899-046-221
; Sequence 221, Application US/09899046
; Publication No. US2003008274A1
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: New sequences of hepatitis C virus

TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/899,046

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362,455

FILING DATE:

INFORMATION FOR SEQ ID NO: 221:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-899-046-221

Query Match 21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRTS 14
||||
Db 4 GRTS 7

RESULT 13

US-09-878-281-219
; Sequence 219, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: New sequences of hepatitis C virus

TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/878,281

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362,455

FILING DATE:

INFORMATION FOR SEQ ID NO: 219:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-878-281-219

Query Match 21.1%; Score 4; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRTS 14
||||
Db 4 GRTS 7

RESULT 14

US-09-878-281-220
; Sequence 220, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: New sequences of hepatitis C virus

TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.

NUMBER OF SEQUENCES: 270

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/878,281

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/362,455

FILING DATE:

INFORMATION FOR SEQ ID NO: 220:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-878-281-220

```

```

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 11 GRTS 14
DB 4 GRTS 7

```

```

RESULT 15
US-09-878-281-221
; Sequence 221, Application US/09878281
; Publication No. US20030032005A1
; GENERAL INFORMATION:

```

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; APPLICANT:
; TITLE OF INVENTION: New sequences of hepatitis C virus
; TITLE OF INVENTION: genotypes for diagnosis, prophylaxis and therapy.
; NUMBER OF SEQUENCES: 270
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/878,281
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/362,455
; FILING DATE:

```

```

; INFORMATION FOR SEQ ID NO: 221:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-878-281-221

```

```

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 11 GRTS 14
DB 4 GRTS 7

```

```

RESULT 16
US-09-572-404B-668
; Sequence 668, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 668
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in FXR1 at 428-437 and may interact with Sequen

```

```

; OTHER INFORMATION: in this patent.
US-09-572-404B-668

```

```

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 GRGR 12
DB 4 GRGR 7

```

```

RESULT 17
US-09-572-404B-670
; Sequence 670, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 670
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in FXR1 at 427-436 and may interact with Sequ
US-09-572-404B-670

```

```

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 GRGR 12
DB 5 GRGR 8

```

```

RESULT 18
US-09-572-404B-672
; Sequence 672, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 672
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in FXR1 at 428-437 and may interact with Sequ
US-09-572-404B-672

```

```

Query Match
Best Local Similarity 100.0%; Score 4; DB 9; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 9 GRGR 12
DB 4 GRGR 7

```

```

RESULT 19

```

```
US-09-572-404B-1028
; Sequence 1028, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1028
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in RPS29 at 42-51 and may interact with Sequence
US-09-572-404B-1028
; OTHER INFORMATION: in this patent.

Query Match
Best Local Similarity 21.1%; Score 4; DB 9; Length 10;
Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
    ||||
Db 2 GRGR 5

RESULT 20
US-09-572-404B-1300
; Sequence 1300, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1300
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in FXR1 at 431-440 and may interact with Sequence
US-09-572-404B-1300
; OTHER INFORMATION: in this patent.

Query Match
Best Local Similarity 21.1%; Score 4; DB 9; Length 10;
Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
    ||||
Db 1 GRGR 4

RESULT 21
US-09-572-404B-1302
; Sequence 1302, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1302
; LENGTH: 10

; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in FXR1 at 482-491 and may interact with Sequ
US-09-572-404B-1302

Query Match
Best Local Similarity 21.1%; Score 4; DB 9; Length 10;
Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
    ||||
Db 6 GRGR 9

RESULT 22
US-09-572-404B-1368
; Sequence 1368, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1368
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in IL9 at 11-20 and may interact with Sequenc
US-09-572-404B-1368

Query Match
Best Local Similarity 21.1%; Score 4; DB 9; Length 10;
Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
    ||||
Db 7 GRGR 10

RESULT 23
US-09-572-404B-1484
; Sequence 1484, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1484
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in RPS29 at 43-52 and may interact with Sequ
US-09-572-404B-1484

Query Match
Best Local Similarity 21.1%; Score 4; DB 9; Length 10;
Pred. No. 4.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GRGR 12
    ||||
```


DB 1 GRGR 4

RESULT 24

US-09-572-404B-1576
 ; Sequence 1576, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProPatent version 1.0
 ; SEQ ID NO 1576
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in KIAA0050 at 529-538 and may interact with Seq
 US-09-572-404B-1576

Query Match 21.1%; Score 4; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
 DB 4 GRGR 7

RESULT 25

US-09-572-404B-1580
 ; Sequence 1580, Application US/09572404B
 ; Publication No. US20030078374A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Proteom Ltd
 ; TITLE OF INVENTION: Complementary peptide ligands from the human genome
 ; FILE REFERENCE: Human patent
 ; CURRENT APPLICATION NUMBER: US/09/572,404B
 ; CURRENT FILING DATE: 2000-05-17
 ; NUMBER OF SEQ ID NOS: 4203
 ; SOFTWARE: ProPatent version 1.0
 ; SEQ ID NO 1580
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 ; FEATURE:
 ; OTHER INFORMATION: sequence located in KIAA0064 at 333-342 and may interact with Seq
 US-09-572-404B-1580

Query Match 21.1%; Score 4; DB 9; Length 10;
 Best Local Similarity 100.0%; Pred. No. 4.6e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRGR 12
 DB 6 GRGR 9

Search completed: May 9, 2003, 16:13:02
 Job time : 51 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:40:19 ; Search time 15 seconds
(without alignments)
121.770 Million cell updates/sec

Title: US-09-674-913A-1
Perfect score: 19
Sequence: 1 NVPGERMGRGRTSKELA 19

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Size: 0

Total number of hits satisfying chosen parameters: 3094

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database: 1: PIR.73:*
2: PIR:*
3: PIR:*
4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4	21.1	11	2	PH0938
2	4	21.1	12	2	S68402
3	4	21.1	16	2	PH0766
4	4	21.1	18	2	B24735
5	4	21.1	20	2	E60894
6	4	21.1	20	2	S33001
7	4	21.1	20	2	S48654
8	3	15.8	10	2	PA0050
9	3	15.8	10	2	A27617
10	3	15.8	10	2	A42089
11	3	15.8	10	2	B24736
12	3	15.8	10	2	P00785
13	3	15.8	11	2	PT0081
14	3	15.8	11	2	S19775
15	3	15.8	11	2	PT0287
16	3	15.8	11	2	I54193
17	3	15.8	11	2	S78422
18	3	15.8	11	2	PH0939
19	3	15.8	11	2	H84082
20	3	15.8	12	2	S26558
21	3	15.8	12	2	S65629
22	3	15.8	12	2	A58501
23	3	15.8	12	2	G49215
24	3	15.8	12	2	T44420
25	3	15.8	12	2	A55837
26	3	15.8	12	2	C30503
27	3	15.8	12	2	PH1587
28	3	15.8	12	2	PH0931
29	3	15.8	13	2	A61288

ALIGNMENTS

30	3	15.8	13	2	PT0331	Ig heavy chain CRD
31	3	15.8	13	2	S54344	glyceraldehyde-3-P
32	3	15.8	14	1	LFECW	trp operon leader
33	3	15.8	14	1	LFEBWC	trp operon leader
34	3	15.8	14	1	LFEBWT	trp operon leader
35	3	15.8	14	2	I51432	histone H4-1 precu
36	3	15.8	14	2	A35377	GTP-binding protei
37	3	15.8	14	2	E90858	trp operon leader
38	3	15.8	14	2	PN0147	omega-gliadine 1 a
39	3	15.8	14	2	PN0151	homeotic protein E
40	3	15.8	14	2	PC1215	metal-binding prot
41	3	15.8	14	2	PL0152	carbonic anhydrase
42	3	15.8	14	2	I64815	T cell receptor al
43	3	15.8	14	2	PH1806	trp operon leader
44	3	15.8	14	2	B85761	H+-transporting tw
45	3	15.8	14	2	F33160	

RESULT 1

PH0938
T-cell receptor beta chain V-D-J region (clone 9) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0938
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0938
A:Molecule type: mRNA
A:Residues: 1-11 <COL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Query Match

Best Local Similarity 100.0%; Score 4; DB 2; Length 11;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RCRT 13

DB 6 RCRT 9

RESULT 2

S68402
NAD(+)-glycohydrolase - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 12-Dec-1997
R:Zhang, J.; Ziegler, M.; Schneider, R.; Klocker, H.; Auer, B.; Schweiger, M.
FEBS Lett. 377, 530-534, 1995
A:Title: Identification and purification of a bovine liver mitochondrial NAD(+)-glyco
A:Reference number: S68402; MUID:96140583; PMID:8549791
A:Accession: S68402
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7,8-12 <ZHA>
C:Genetics:
A:Genome: nuclear
C:Keywords: mitochondrion; NAD

Query Match

Best Local Similarity 100.0%; Score 4; DB 2; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 KEIA 19

DB 8 KEIA 11

RESULT 3
PH0766
T-cell receptor beta chain (J3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0766
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-T
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078446; PMID:1836010
A:Accession: PH0766
A:Molecule type: mRNA
A:Residues: 1-16 <CAMS>
A:Cross-references: EMBL:X60860; NID:952745; PIDN:CAA43250.1; PID:952746
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 21.1%; Score 4; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 GRGT 13
1111
Db 6 GRGT 9

RESULT 4
B24735
glutathione transferase (EC 2.5.1.18) 1-2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 18-Jun-1993
C:Accession: B24735
R:Manneville, B.; Alin, P.; Guttenberg, C.; Jensen, H.; Tahir, M.K.; Warholm, M.; Jorvæ
Proc. Natl. Acad. Sci. U.S.A. 82, 7202-7206, 1985
A:Title: Identification of three classes of cytosolic glutathione transferase common to
A:Reference number: A24735; MUID:86042634; PMID:3864155
A:Accession: B24735
A:Molecule type: protein
A:Residues: 1-18 <MAN>
C:Superfamily: glutathione transferase
C:Keywords: transferase

Query Match 21.1%; Score 4; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GRGR 12
1111
Db 11 GRGR 14

RESULT 5
E60894
crystallin - Pacific cuttlefish (fragment)
C:Species: Sepia esculenta (Pacific cuttlefish)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 02-Jun-1994
C:Accession: E60894
R:Chion, S.H.
J. Protein Chem. 7, 527-534, 1988
A:Title: The protein sequence homology of gamma-crystallins among major vertebrate class
A:Reference number: A60894; MUID:89351593; PMID:3255376
A:Accession: E60894
A:Molecule type: protein
A:Residues: 1-20 <CHT>
C:Superfamily: glutathione transferase
C:Keywords: eye lens

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GRGR 12

Db 10 GRGR 13
1111
RESULT 6
S33001
hypothetical protein - human herpesvirus 4
C:Species: human herpesvirus 4, Epstein-Barr virus
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C:Accession: S33001
R:Farrell, P.J.
submitted to the EMBL Data Library, March 1988
A:Reference number: S32973
A:Accession: S33001
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <FAR>
A:Cross-references: EMBL:V01555; NID:959074; PIDN:CAA24847.1; PID:91334861

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 RTSS 15
1111
Db 9 RTSS 12

RESULT 7
S48654
Plasmeprin II - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C>Date: 15-Jul-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jun-2000
C:Accession: S48654
R:Hill, J.; Tyas, L.; Phylip, L.H.; Kay, J.; Dunn, B.M.; Berry, C.
FEBS Lett. 352, 155-158, 1994
A:Title: High level expression and characterisation of Plasmeprin II, an aspartic pro
A:Reference number: S48654; MUID:95010698; PMID:7925966
A:Accession: S48654
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <HIL>

Query Match 21.1%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 MGRG 11
1111
Db 10 MGRG 13

RESULT 8
PA0050
protein OA100052 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:Accession: PA0050; PA0107
R:Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensi
A:Reference number: PA0001
A:Accession: PA0050
A:Molecule type: protein
A:Residues: 1-10 <KAM>
R:Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A:Reference number: PA0107
A:Accession: PA0107
A:Molecule type: protein
A:Residues: 1-10 <KAM>
A:Experimental source: root

Query Match 15.8%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0;

OY 13 TSS 15
|||
Db 2 TSS 4

RESULT 9

A27617
triose-phosphate isomerase (EC 5.3.1.1) - curled-leaved tobacco (fragment)
C:Species: Nicotiana glauca (curled-leaved tobacco)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 28-Apr-1993
C:Accession: A27617
R:Baum, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandeckerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A:Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
C:Accession: A27617
A:Residues: 1-10 <BAU>
C:Keywords: gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomerase; pento

Query Match 15.8%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
|||
Db 1 GRT 3

RESULT 10

A42089
transcription factor I-POU protein, alternative splice form - fruit fly (Drosophila mela
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
C:Accession: A42089
R:Treacy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.G.
Cell 68, 491-505, 1992
A:Title: Twin of I-POU: a two amino acid difference in the I-POU homeodomain distinguish
A:Reference number: A42089; MIMD:92154665; PMID:1346754
A:Accession: A42089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <TRE>
C:Cross-references: GB:S82271; NID:q245517; PID:q245518
C:Keywords: sequence extracted from NCBI backbone (NCBIN:82267, NCBI:82271, NCBI:82273)
A:Gene: FlyBase:IPou
A:Cross-references: FlyBase:FBgn0004418

Query Match 15.8%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 RTS 14
|||
Db 7 RTS 9

RESULT 11

B24736
inhibin beta-B chain - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 30-Sep-1993
C:Accession: B24736
R:Liing, N.; Ying, S.Y.; Ueno, N.; Esch, F.; Denotroy, L.; Guillemin, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 7217-7221, 1985
A:Reference number: A24736; MIMD:86042637; PMID:3864157
A:Accession: B24736
A:Status: preliminary

A:Molecule type: protein
A:Residues: 1-10 <LIN>

Query Match 15.8%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
|||
Db 6 GRT 8

RESULT 12

P00785
NADH dehydrogenase (EC 1.6.99.3) 27K chain - fava bean mitochondrion (fragment)
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
C:Accession: P00785
R:Letierme, S.; Boultry, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NA
A:Reference number: P00775; MIMD:94151437; PMID:8108509
A:Accession: P00785
A:Molecule type: protein
A:Residues: 1-10 <LET>
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the
ranging from 5K to 75K.
C:Keywords: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone
A:Genome: mitochondrion
C:Genetics:
A:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 15.8%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPG 4
|||
Db 3 VPG 5

RESULT 13

PT0081
protein OA300023 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse ear cress)
C:Date: 07-Feb-1996 #sequence_revision 19-Apr-1996 #text_change 24-Nov-1999
C:Accession: PT0081
R:Tsugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.
submitted to JIPID, December 1995
A:Description: Two dimensional electrophoresis of plant proteins and standardization
A:Reference number: PM0173
A:Accession: PT0081
A:Molecule type: protein
A:Residues: 1-11 <TSU>
A:Experimental source: Leaf
C:Keywords: acetylated amino end
F:1/Modified site: acetylated amino end (Ser) #status experimental

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SKE 17
|||
Db 1 SKE 3

RESULT 14

S19775
wound-induced protein - tomato (fragment)
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Sep-1997

C:Accession: S19775
R:Parsons, B.L.
submitted to the EMBL Data Library, May 1991
A:Reference number: S19773
A:Accession: S19775
A:Molecule type: mRNA
A:Residues: 1-11 <PAR>
A:Cross-references: EMBL:X59884; NID:g19323; PID:g19324

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSK 16
|||
Db 3 SSK 5

RESULT 15

PM0287
heavy chain CRD3 region (clone 4-103) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0287
R:Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0287
A:Molecule type: DNA
A:Residues: 1-11 <YAM>
A:Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
|||
Db 5 GRT 7

RESULT 16

I54193
Rhesus blood group CcEe protein - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C:Accession: I54193
R:Peril-Zahar, B.; Le Van Kim, C.; Rouillac, C.; Raynal, V.; Cartron, J.P.; Collin, Y.
Genomics 19, 68-74, 1994
A:Title: Organization of the gene (RHEC) encoding the human blood group RHCcEe antigens
A:Reference number: I54193; MUID:94245182; PMID:8188244
A:Accession: I54193
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-11 <RES>
A:Cross-references: GB:S70456; NID:g546795; PIDN:AA014061.1; PID:g4261761
C:Genetics:
A:Gene: GDB:RHCE
A:Cross-references: GDB:229957; OMIM:111700
A:Map position: 1p36.2-1p34

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSK 16
|||
Db 2 SSK 4

RESULT 17

S78422

ribosomal protein S20, mitochondrial [validated] - rat (tentative sequence) (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C:Accession: S78422
R:Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A:Reference number: S78411
A:Accession: S78422
A:Molecule type: protein
A:Residues: 1-11 <GOL>
A:Note: the protein is designated as mitochondrial ribosomal protein S20
C:Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ELA 19
|||
Db 4 ELA 6

RESULT 18

PH0939
T-cell receptor beta chain V-D-J region (clone 10) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0939
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental alle
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0939
A:Molecule type: mRNA
A:Residues: 1-11 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SSK 16
|||
Db 3 SSK 5

RESULT 19

H84082
hypothetical protein BH3464 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C:Accession: H84082
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; H
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a
A:Reference number: AB3650; MUID:20512582; PMID:11058132
A:Accession: H84082
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <STO>
A:Cross-references: GB:AP001518; GB:BA000004; NID:g10175792; PIDN:BA07183.1; GSPDB:G
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH3464

Query Match 15.8%; Score 3; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 KEL 18
|||

Db 4 KEL 6

RESULT 20

S26558
T-cell receptor beta chain (clone CW3/5B8) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
C:Accession: S26558
R:Casanova, J.L.; Cerottini, J.C.; Mathes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: S26558
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>
A:Experimental source: EMBL:X68008
C:Suprafamily: immunoglobulin V region; immunoglobulin homology
Keywords: T-cell receptor

Query Match

Best Local Similarity 15.8%; Score 3; DB 2; Length 12;
100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 SKK 16

Db 3 SSK 5

RESULT 21

S65629
protoporphyrinogen oxidase (EC 1.3.3.4) - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 26-May-2000
C:Accession: S65629
R:Takekoshi, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Nishimura, K.; Ino
Eur. J. Biochem. 230, 760-765, 1995
A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m
A:Reference number: S65629; MUID:95331315; PMID:7607249
A:Accession: S65629
A:Molecule type: protein
A:Residues: 1-12 <TAK>
C:Genetics:
A:Genome: nuclear
C:Function:
A:Pathway: heme biosynthesis; porphyrin biosynthesis
Suprafamily: phytoene dehydrogenase
Keywords: heme biosynthesis; mitochondrion; oxidoreductase; porphyrin biosynthesis

Query Match

Best Local Similarity 15.8%; Score 3; DB 2; Length 12;
100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GRT 13

Db 1 GRT 3

RESULT 22

A58501
24K kidney and bladder stone protein 1 - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: A58501
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: A58501
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>

A:Experimental source: human kidney and bladder stones
A>Note: tentative identification of 2-Ser

Query Match

Best Local Similarity 15.8%; Score 3; DB 2; Length 12;
100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 SKE 17

Db 2 SKE 4

RESULT 23

G49215
urease (EC 3.5.1.5) small subunit urea - Helicobacter felis (fragment)
C:Species: Helicobacter felis
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-1995
C:Accession: G49215
R:Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
A:Title: Purification and characterization of the urease enzymes of Helicobacter spec
A:Reference number: A49215; MUID:93084378; PMID:1452359
A:Accession: G49215
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <TUR>
A:Experimental source: ATCC 49179
A>Note: Sequence extracted from NCBI backbone (NCBIP:119489)
C:Keywords: hydrolase

Query Match

Best Local Similarity 15.8%; Score 3; DB 2; Length 12;
100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 KEL 18

Db 6 KEL 8

RESULT 24

T44420
hypothetical protein [imported] - Bacillus stearothermophilus (fragment)
C:Species: Bacillus stearothermophilus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C:Accession: T44420
R:Vlasova, H.; Krasny, L.; Fucik, V.; Jonak, J.
submitted to the EMBL Data Library, September 1997
A:Description: The pyrb gene coding for the large subunit of carbamoylphosphate synt
A:Reference number: Z22760
A:Accession: T44420
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-12 <VLA>
A:Cross-references: EMBL:AJ001805; PIDN:CAA05021.1
A:Experimental source: strain CCM 2184
A>Note: ORF2
C:Genetics:

Query Match

Best Local Similarity 15.8%; Score 3; DB 2; Length 12;
100.0%; Pred. No. 4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ERM 8

Db 5 ERM 7

RESULT 25

A55837
5-aminimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminimidazo
C:Species: Gallus gallus (chicken)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C:Accession: A55837

R:Firestone, S.M.; Davison, V.J.
 Biochemistry 33, 11917-11926, 1994
 A:Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal
 A:Reference number: A55837; MUID:95001903; PMID:7918410
 A:Accession: A55837
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <FIR>

Query Match 15.8%; Score 3; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 ELA 19
 DB 5 ELA 7

Search completed: May 9, 2003, 16:06:07
 Job time : 18 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:39:44 ; Search time 10 seconds
(without alignments)

78.805 Million cell updates/sec

Title: US-09-674-913A-1

Perfect score: 19
Sequence: 1 NVPGHERMGRTSSKELA 19

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Database size: 0

Total number of hits satisfying chosen parameters: 916

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	26.3	15	1 UC08_MAIZE	P80614 zea mays (m
2	3	15.8	10	1 TPIS_NICPL	P19118 nicotiana p
3	3	15.8	14	1 ADF_TEMO	P82865 tenebrio mo
4	3	15.8	14	1 LPW_CITFR	P03056 citrobacter
5	3	15.8	14	1 LPW_ECOLI	P03053 escherichia
6	3	15.8	14	1 LPW_SALTY	P03054 salmonella
7	3	15.8	14	1 NEJ2_FASHE	P80526 fasciola he
8	3	15.8	14	1 PPK6_PERAM	P82693 periplaneta
9	3	15.8	14	1 TKNI_SCHGR	P82470 schistocerc
10	3	15.8	15	1 DCNM_PSECH	P19817 pseudomonas
11	3	15.8	15	1 ONCI_ONCMY	P83287 oncorhynch
12	3	15.8	17	1 MPMX_SOLTU	P80501 solanum tub
13	3	15.8	16	1 VESP_VESMC	P57672 vespula mac
14	3	15.8	18	1 CPAX_BOVIN	P22779 bos taurus
15	3	15.8	18	1 GOME_ACAGO	P82358 acanthoscur
16	3	15.8	19	1 FTIB_HORSE	P14471 equus cabal
17	3	15.8	19	1 MIFB_TRIMR	P81530 trichuris m
18	3	15.8	20	1 ALAT_PIG	P13191 sus scrofa
19	3	15.8	20	1 EFTU_MYCST	P81407 mycoplasma
20	3	15.8	20	1 TTRA_ALBUJ	P24925 albizzia ju
21	3	15.8	20	1 LYC_FELCA	P37155 felis silve
22	3	15.8	20	1 MIF_PIG	P80928 sus scrofa
23	3	15.8	20	1 PORC_METTM	P80902 methanobact
24	3	15.8	20	1 PSBW_WHEAT	P55667 triticum ae
25	3	15.8	20	1 RIPP_CUCPE	P80750 cucurbita p
26	3	15.8	20	1 SAMP_PLEPL	P20677 pleurocete
27	3	15.8	10	1 AMPN_HELIAM	P81731 helicoverpa
28	3	10.5	10	1 BPP_VIPAS	P31511 vipera aspi
29	2	10.5	10	1 BRK_ONCMY	Q9p21 oncorhynch
30	2	10.5	10	1 COXN_ONCMY	P80331 oncorhynch
31	2	10.5	10	1 COXK_ONCMY	P80332 oncorhynch
32	2	10.5	10	1 COXO_PAN	P80432 rattus norv
33	2	10.5	10	1 COXO_THUOB	P80982 thunnus obe

34	2	10.5	10	1 COXO_RABIT	P80336 oryctolagus
35	2	10.5	10	1 EST_LACCA	P81758 lactobacilli
36	2	10.5	10	1 FARP_MYTED	P42560 mytilus edu
37	2	10.5	10	1 GAUJ_HUMAN	P01358 homo sapien
38	2	10.5	10	1 GLEM_HUMAN	P02728 homo sapien
39	2	10.5	10	1 GONI_ALLAM	P37041 alligator m
40	2	10.5	10	1 GONI_CHEPR	P80677 chelyosoma
41	2	10.5	10	1 GONI_CLUPA	P81749 clupea pall
42	2	10.5	10	1 GONI_PETMA	P04378 petromyzon
43	2	10.5	10	1 GON2_CHEPR	P80678 chelyosoma
44	2	10.5	10	1 GON2_CHICK	P37043 gallus gall
45	2	10.5	10	1 GON3_ONCKE	P20367 oncorhynch

ALIGNMENTS

RESULT 1					
ID	UC08_MAIZE	STANDARD;	PRT;	15 AA.	
AC	P80614;				
DT	01-OCT-1996 (Rel. 34, Created)				
DT	01-OCT-1996 (Rel. 34, Last sequence update)				
DT	15-JUL-1999 (Rel. 38, Last annotation update)				
DE	Unknown protein from 2D-page of etiolated coleoptile (Spot 159)				
DE	(Fragment).				
OS	Zea mays (Maize).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;				
OC	Palloidsae; Andropogoneae; Zea.				
OX	NCBI_TaxID=4577;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Coleoptile;				
RA	Touzet P., Riccardi F., Morin C., Damerival C., Huet J.-C.,				
RA	Penholet J.-C., Zivy M., de Vienne D.,				
RT	"The maize two dimensional gel protein database: towards an integrated				
RT	genome analysis program."				
RL	Theor. Appl. Genet. 93:997-1005(1996).				
CC	-1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN				
CC	PROTEIN IS: 6.4, ITS MW IS: 38.8 KDa.				
CC	-1- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE				
CC	FAMILY.				
DR	Maize-2DPAGE; P80614; COLEOPTILE.				
DR	MaizeDB; 123934; "				
FT	NON_TER	1			
FT	NON_TER	15			
SO	SEQUENCE	15 AA;	1785 MW;	1978B1D5AB4DDEBD CRC64;	
Query Match					
Best Local Similarity 26.3%; Score 5; DB 1; Length 15;					
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	2 VPGHE 6				
DB	11 VPGHE 15				
RESULT 2					
ID	TPIS_NICPL	STANDARD;	PRT;	10 AA.	
AC	P19118;				
DT	01-NOV-1990 (Rel. 16, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Tirosephosphate isomerase, cytosolic (EC 5.3.1.1) (TIM) (Fragment).				
OS	Nicotiana glauca (Leadwort-leaved tobacco); Tracheophyta;				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
OC	Assteridae; euasterids I; Solanales; Solanaceae; Nicotiana.				
OX	NCBI_TaxID=4092;				
RN	[1]				
RP	SEQUENCE.				

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RA Bauw G., de Loose M., Inze D., van Montagu M., Vandekerckhove J.;
RT "Alterations in the phenotype of plant cells studied by NH2-terminal
RT amino acid-sequence analysis of proteins electrophoretically
RT dimensional gel-separated total extracts.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4806-4810(1987).
CC -1- CATABOLIC ACTIVITY: D-glycerolaldehyde 3-phosphate - glyceralone
CC phosphate.
CC -1- PATHWAY: PLAYS AN IMPORTANT ROLE IN SEVERAL METABOLIC PATHWAYS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC -1- MISCELLANEOUS: IN PLANTS, THERE ARE TWO TYPES OF TPIS, CYTOSOLIC
CC AND PLASTID.
CC -1- SIMILARITY: BELONGS TO THE TRIOSEPHOSPHATE ISOMERASE FAMILY.
DR PIR: A27617; A27617.
DR InterPro: IPR000652; Triophos_ismrse.
DR PROSITE: PS00171; TIM; PARTIAL.
KW Isomerase; Glycolysis; Gluconeogenesis; Fatty acid biosynthesis;
KW Pentose shunt.
FT NON_PRR 10 10
SO SEQUENCE 10 AA; 1140 MW; 80B9D37862C9C9D1 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 10;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRT 13
DB 1 GRT 3

RESULT 3
ADF_TENMO STANDARD: PRT; 14 AA.
ID ADF_TENMO
AC P82965;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Antidiuretic factor (ADF) (Antidiuretic hormone A) (ADHA).
OS Tenebrio molitor (Yellow mealworm).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga;
OC Cucujiformia; Tenebrionidae; Tenebrio.
OX NCBI_TaxID=7067;
RN [1]
RP SEQUENCE, FUNCTION, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE-Head;
RX MEDLINE=21642653; PubMed=11756661;
RA Eigenheer R.A., Nicolson S.W., Schegg K.M., Hull J.J., Schooley D.A.;
RA "Identification of a potent antidiuretic factor acting on beetle
RA Malpighian tubules.";
Proc. Natl. Acad. Sci. U.S.A. 99:84-89(2002).
CC -1- FUNCTION: Strong inhibitor of fluid secretion and inhibits fluid
CC tubules. Uses cGMP as a second messenger and inhibits fluid
CC production by decreasing cAMP concentration.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=1541.58; METHOD=MALDI.
CC -1- SIMILARITY: STRONG, TO THE C-TERMINAL OF T. MOLITOR CUTICULAR
CC PROTEIN LPCP29.
KW Neuropeptide; Hormone.
SO SEQUENCE 14 AA; 1543 MW; F49C91A3F16F43D1 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PGH 5
DB 5 PGH 7

RESULT 4
LFW_CITFR STANDARD: PRT; 14 AA.
ID LFW_CITFR

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AC P03056;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-MAY-1991 (Rel. 18, Last annotation update)
DE TTP operon leader peptide.
GN TTP.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Citrobacter
OX NCBI_TaxID=546;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83007061; PubMed=6749821;
RA Blumenberg M., Yanofsky C.;
RT "Evolutionary divergence of the Citrobacter freundii tryptophan
RT operon regulatory region: comparison with other enteric bacteria.";
RL J. Bacteriol. 152:57-66(1982).
CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS
CC OF TRYPTOPHAN.
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CC -----
CC EMBL: J01557; -: NOT_ANNOTATED_CDS.
DR PIR: A03592; LFEHWC.
KW Tryptophan biosynthesis; Leader peptide.
SO SEQUENCE 14 AA; 1720 MW; 5B792A473E8048E7 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 14;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 RTS 14
DB 12 RTS 14

RESULT 5
LFW_ECOLI STANDARD: PRT; 14 AA.
ID LFW_ECOLI
AC P03053;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE TTP operon leader peptide.
GN TTP OR TRPE OR B1265 OR 22545 OR ECS1837.
OS Escherichia coli, and
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=82150258; PubMed=7038627;
RA Yanofsky C., Platt T., Crawford I.P., Nichols B.P., Christie G.E.,
RA Horowitz H., van Cleemput M., Wu A.M.;
RT "The complete nucleotide sequence of the tryptophan operon of
RT Escherichia coli.";
RL Nucleic Acids Res. 9:6647-6668(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=76240562; PubMed=781271;
RA Squires C., Lee F., Bertrand K., Squires C.L., Bronson M.J.,
RA Yanofsky C.;
RT "Nucleotide sequence of the 5' end of tryptophan messenger RNA of
RT Escherichia coli.";
RL J. Mol. Biol. 103:351-381(1976).
RN [3]

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RP SEQUENCE FROM N.A.
RX MEDLINE=80101455; PubMed=118451;
RA Oxender D.L., Zurawski G., Yanofsky C.;
RT "Attenuation in the Escherichia coli tryptophan operon: role of RNA
RT secondary structure involving the tryptophan codon region.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:5524-5528(1979).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX MEDLINE=21074933; PubMed=11206551;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamous K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
RL Nature 409:529-533(2001).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=O157:H7 / RIMD 0509952;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han G.-G., Ohtsudo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
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DR EMBL: J01714; AAS7296.1; -
DR EMBL: A04494; CAA00361.1; -
DR EMBL: AE000224; AAC74347.1; -
DR EMBL: AE005380; AAG56550.1; -
DR EMBL: AF002556; BAB35260.1; -
DR PIR: A03589; LEFCW.
DR EcoGene: EG11274; trpL.
DR Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA: 1723 MW: 5879306E3B804A37 CRC64.

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Query Match 15.8%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 12 RTS 14
DB 12 RTS 14

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RESULT 6
LPM_SALTY STANDARD; PRT; 14 AA.
AC P03054;

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DT 21-JUN-1986 (Rel. 01, Created)
DT 21-JUN-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TTP operon leader peptide.
GN TRPL OR TRPEE OR SYM1722.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=7816931; PubMed=351195;
RA Lee F., Bertrand K., Bennett G.N., Yanofsky C.;
RT "Comparison of the nucleotide sequences of the initial transcribed
RT regions of the tryptophan operons of Escherichia coli and Salmonella
RT typhimurium.";
RL J. Mol. Biol. 121:193-217(1978).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McCelland M., Sanderson K.E., Spleth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2.";
RL Nature 413:852-856(2001).
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DR EMBL: M24960; -; NOT_ANNOTATED_CDS.
DR EMBL: AE008776; AAL20640.1; -
DR PIR: A03590; LEFBWT.
DR StyGene: SG10400; trpL.
KW Tryptophan biosynthesis; Leader peptide; Complete proteome.
SQ SEQUENCE 14 AA: 1635 MW: 49F22A47362248E7 CRC64.

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Query Match 15.8%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 12 RTS 14
DB 12 RTS 14

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RESULT 7
NEJ2_FASHE STANDARD; PRT; 14 AA.
AC P80526;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Newly excysted juvenile protein 2 (Fragment).
OS Fasciola hepatica (liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fascioloidae; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalcic J., Ashman K., Meusen E.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile

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RT proteins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT THE NEWLY EXCYSTED JUVENILE
STAGE.
CC RT
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1581 MW; 9E0F0090CC8C0DF1 CRC64;
Query Match 15.8%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 11 GRT 13
DB 5 GRT 7
RESULT 8
PK6_PERAM STANDARD; PRT; 14 AA.
AC P82693;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DE Pyrokinin-6 (Pea-PK-6) (FXPRL-amide).
OS Periplaneta americana (American cockroach).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
OC Blattellidae; Blattidae; Periplaneta.
OC NCBI_TaxID=6978;
RN [1]
RP SQUENCE. FUNCTION: TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Abdominal perisymphathetic organs, and Corpora cardiaca;
MDLINE=20189894; PubMed=10723010;
RX MEDLINE=20189894; PubMed=10723010;
RA Predel R., Eckert M.;
RT "Tagma-specific distribution of FXPRLamides in the nervous system of
the American cockroach."
RL J. Comp. Neurol. 419:352-363(2000).
CC -1- FUNCTION: SHOWS A WEAKLY MYOACTIVE ACTION.
CC -1- TISSUE SPECIFICITY: CORPORA ALATA AND TO A LESSER EXTENT IN
ABDOMINAL PERISYPHATHETIC ORGANS.
CC -1- MASS SPECTROMETRY: MW=1590.8; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE PYROKININ FAMILY.
DR InterPro: IPR001484; Pyrokinin.
DR PROSITE: PS00539; PYROKININ; 1.
KW Amidation; Pyrokinin.
FT MOD_RES 14 14 AMIDATION
SQ SEQUENCE 14 AA; 1592 MW; 3966CC3FF384A998 CRC64;
Query Match 15.8%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPG 4
DB 5 VPG 7
RESULT 9
TKN1_SCHGR STANDARD; PRT; 14 AA.
AC P82470;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tachykinin-1 (Scg-midgut-TK).
OS Schistocerca gregaria (Desert locust).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OC Acridomorpha; Acridoidea; Acrididae; Cyrtacanthacridinae;
OC Schistocerca.
OC NCBI_TaxID=7010;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Midgut;
RX MEDLINE=20050081; PubMed=10581195;
RA Veelaert D., Baggerman G., Derna R., Waelkens E., Meusen T.,
RA Vande Water G., De Loof A., Schoofs L.;
RT "Identification of a new tachykinin from the midgut of the desert
locust, Schistocerca gregaria, by ESI-Qq-oe-TOF mass spectrometry."
RL Biochem. Biophys. Res. Commun. 266:237-242(1999).
CC -1- FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY
OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
CC -1- TISSUE SPECIFICITY: MIDGUT.
CC -1- MASS SPECTROMETRY: MW=1493.79; METHOD=Electrospray.
CC -1- SIMILARITY: SIMILAR TO THE COCKROACH LEMTRP 3, A TACHYKININ-
RELATED PEPTIDE ALSO CONFINED TO THE MIDGUT.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 14 14 AMIDATION
SQ SEQUENCE 14 AA; 1496 MW; CAC578C0169FC72 CRC64;
Query Match 15.8%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VPG 4
DB 7 VPG 9
RESULT 10
DCM_PSECH STANDARD; PRT; 15 AA.
AC P19917;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbon monoxide dehydrogenase medium chain (EC 1.2.99.2) (CO
dehydrogenase subunit M) (CO-DH M) (Fragment).
GN COTM.
OS Pseudomonas carboxydohydrogena.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Bradyrhizobium group.
OC NCBI_TaxID=290;
RN [1]
RP SEQUENCE
RX MEDLINE=90055678; PubMed=2818128;
RA Krait M., Hugendieck I., Herwig S., Meyer O.;
RT "Homology and distribution of CO dehydrogenase structural genes in
RT carboxydohydrogenic bacteria."
RL Arch. Microbiol. 152:335-341(1989).
CC -1- FUNCTION: Catalyzes the oxidation of carbon monoxide to carbon
dioxide.
CC -1- CATALYTIC ACTIVITY: CO + H(2)O + acceptor = CO(2) + reduced
acceptor.
CC -1- COFACTOR: FAD.
CC -1- SUBUNIT: CONSISTS OF THREE POLYPEPTIDE CHAINS: LARGE, MEDIUM, AND
SMALL.
DR PIR; P10143; P10143.
KW Oxidoreductase; Flavoprotein; FAD.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1815 MW; 90508CF93E739D63 CRC64;
Query Match 15.8%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 PGH 5
DB 4 PGH 6
RESULT 11
ONCL_ONCMY STANDARD; PRT; 15 AA.
AC P83287;
15-JUN-2002 (Rel. 41, Created)

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DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Oncorhynchus 1 (Fragment).
OC Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Actinopterygii: Neopterygii: Teleostei: Euteleostei:
OC Proteocephali: Pterogota: Neoptera: Hymenoptera: Apocrita:
OC NCBI_TaxID=8022;
RN NCBI_TaxID=8022;
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin;
RA "Purification and N-terminal sequencing of a 3 kDa antibacterial
peptide from skin secretions of rainbow trout."
RL Submitted (MAY-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Has antibacterial activity against Gram-positive
bacterium P. citreus.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC Antibiotic.
FT UNSURE 4 4 OR G.
FT UNSURE 9 9 OR T.
SQ SEQUENCE 15 AA: 1601 MW: 43C25028DBC12B7C CRC64;
Query Match 15.8%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 17 ELA 19
Db 11 ELA 13

RESULT 12
MMPX_SOLTU STANDARD: PRT: 16 AA.
AC P80501;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Unidentified mitochondrial matrix protein (Frigment).
OS Solanum tuberosum (Potato).
OC Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
OC Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots:
OC Asteridae: easterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
[1]
SEQUENCE.
RC TISSUE=Tuber;
RA MEDLINE=97077345; PubMed=8919912;
RA Jansch L., Kuft V., Schmitz U.K., Braun H.P.;
RT "New insights into the composition, molecular mass and stoichiometry
of the protein complexes of plant mitochondria."
RL Plant J. 9:357-368(1996).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC Mitochondrion.
FT NON_TER 16
SQ SEQUENCE 16 AA: 1768 MW: C58D4DB48A18B8D CRC64;

Query Match 15.8%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 NVP 3
Db 3 NVP 5

RESULT 13
VESP_VESMC STANDARD: PRT: 17 AA.
ID VESP_VESMC
AC P57672;

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DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Vespulakinin 1 (Contamin: Vespulakinin 2).
OS Vespula maculifrons (Eastern yellow jacket) (Wasp).
OC Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda:
OC Insecta: Pterygota: Neoptera: Endopterygota: Hymenoptera: Apocrita:
OC Aculeata: Vespidae: Vespinae: Vespula.
OX NCBI_TaxID=7453;
RN NCBI_TaxID=7453;
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=76114777; PubMed=1247511;
RA Yoshida H., Geller R.G., Pisano J.J.;
RT "Vespulakinin: new carbohydrate-containing bradykinin derivatives."
RL Biochemistry 15:61-64(1976).
RN [2]
RP SYNTHESIS.
RX MEDLINE=88057857; PubMed=3679673;
RX Rocchi R., Blondi L., Filira F., Scolaro B.;
RT "Synthesis, conformation, and biological activity of the carbohydrate-
free vespulakinin 1."
RL Int. J. Pept. Protein Res. 30:240-256(1987).
CC -1- FUNCTION: SMOOTH MUSCLE CONTRACTION.
CC -1- SUBCELLULAR LOCATION: SECRETED; WASP VENOM RESERVOIRS.
CC -1- SIMILARITY: BELONGS TO THE BRADYKININ FAMILY.
KW Bradykinin; Vasodilator; Venom; Glycoprotein.
FT PEPTIDE 17 VESPUKAKININ 1.
FT CARBOHYD 3 17 VESPUKAKININ 2.
FT CARBOHYD 3 3 O-LINKED (GALNAC. . .)
FT CARBOHYD 4 4 O-LINKED (GALNAC. . .)
SQ SEQUENCE 17 AA: 1960 MW: 58B2CBA864122323 CRC64;
Query Match 15.8%; Score 3; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 10 RGR 12
Db 7 RGR 9

RESULT 14
CPAX_BOVIN STANDARD: PRT: 18 AA.
ID CPAX_BOVIN
AC P22779;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cytochrome P450 2A (OLF2) (Olfactive) (P52) (EC 1.14.14.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Ruminantia: Pecora: Bovidae:
OC Bovidae: Bovinae: Bos.
OX NCBI_TaxID=9913;
[1]
SEQUENCE.
RP MEDLINE=91027757; PubMed=2121272;
RA Lazard P., Tal N., Rubinstein M., Khen M., Lancet D., Zupko K.;
RT "Identification and biochemical analysis of novel olfactory-specific
cytochrome P-450IIA and UDP-glucuronosyl transferase."
RL Biochemistry 29:7433-7440(1990).
CC -1- FUNCTION: CYTOCHROMES P450 ARE A GROUP OF HEME-THIOLATE
MONOOXYGENASES. IN LIVER MICROSOMES, THIS ENZYME IS INVOLVED IN AN
NADPH-DEPENDENT ELECTRON TRANSPORT PATHWAY. IT OXIDIZES A VARIETY
OF STRUCTURALLY UNRELATED COMPOUNDS, INCLUDING STEROIDS, FATY
ACIDS, AND XENOBIOTICS.
CC -1- CATALYTIC ACTIVITY: RH + reduced flavoprotein + O(2) = ROH +
oxidized flavoprotein + H(2)O.
CC -1- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
PR: A35704; A35704.
DR InterPro: IPR001128; Cytochrome_P450.

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DR PROSITE: PS00086; CYTOCHROME P450; PARTIAL.
 KW Oxidoreductase; Monooxygenase; Electron transport; Membrane; Heme;
 KM Microsome; Endoplasmic reticulum; Olfaction.
 FT NON_TER 1
 FT VARIANT 6 6 G -> D.
 FT VARIANT 11 11 A -> E.
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA: 2058 MW: F80746F76CDD77FF CRC64;
 Query Match 15.8%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 16 KEL 18
 DB 13 KEL 15
 RESULT 15
 GOME_ACAGO STANDARD; PRT; 18 AA.
 P82358;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gomesin.
 OS Acanthoscurria gomesiana.
 CC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 CC Mygalomorphae; Theraphosidae; Acanthoscurria.
 OX NCBI_TaxID=115339;
 RN (1)
 RP SEQUENCE, MASS SPECTROMETRY, ACTIVITY, TISSUE SPECIFICITY, AMIDATION,
 RP AND DISULFIDE BONDS.
 RC TISSUE-Hemocyte;
 RX MEDLINE=20517902; PubMed=10942757;
 RA Silva P.I., Jr., Dalfre S., Bulet P.;
 RT "Isolation and characterization of gomesin, an 18-residue cysteine-
 rich defense peptide from the spider Acanthoscurria gomesiana
 RT hemocytes with sequence similarities to horseshoe crab antimicrobial
 RT peptides of the tachyplesin family.";
 RL J. Biol. Chem. 275:33464-33470(2000).
 CC -i- FUNCTION: ACTIVE AGAINST SEVERAL GRAM-POSITIVE BACTERIA SUCH AS
 CC BACILLUS SPP, STAPHYLOCOCCUS SPP AND E. FAECALIS, SEVERAL GRAM-
 CC NEGATIVE BACTERIA SUCH AS E. COLI, K. PNEUMONIAE, P. AERUGINOSA AND
 CC SALMONELLA SPP, FILAMENTOUS FUNGI SUCH AS N. CRASSA, T. VIRIDAE
 CC AND YEASTS SUCH AS C. ALBICANS. IT IS ACTIVE AGAINST THE PARASITE
 CC L. AMAZONENSIS AS WELL. IT SHOWS HEMOLYTIC ACTIVITY.
 CC -i- TISSUE SPECIFICITY: HEMOCYTES.
 CC -i- MASS SPECTROMETRY: MW=2270.4; METHOD=MALDI.
 CC Amidation; Antibiotic; Fungicide; Hemolysis.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 18 18 AMIDATION.
 FT DISULFID 2 15
 FT DISULFID 6 11
 SQ SEQUENCE 18 AA: 2293 MW: 25ED499784908913 CRC64;
 Query Match 15.8%; Score 3; DB 1; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 RGR 12
 DB 16 RGR 18
 RESULT 16
 FTBB_HORSE STANDARD; PRT; 19 AA.
 AC P14471;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).

GN FCB.
 OS Equus caballus (Horse), and
 OS Equus asinus (Donkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796, 9793;
 RN (1)
 RP SEQUENCE.
 RC SPECIES-Horse;
 RA Blomback B., Blomback M., Grondahl N.J.;
 RT "Studies on fibrinopeptides from mammals.";
 RL Acta Chem. Scand. 19:1789-1791(1965).
 RN [2]
 RP SEQUENCE.
 RC SPECIES-E. asinus;
 RA Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
 RT "Structure of fibrinopeptides-its relation to enzyme specificity and
 RT phylogeny and classification of species.";
 RL Ark. Kemi 25:411-428(1966).
 CC -i- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -i- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -i- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 DR InterPro: IPR002181; Fibrinogen_C.
 DR PROSITE: PS00514; FIBRIN_Ac_C-DOMAIN; PARTIAL.
 KW Blood coagulation; Plasma; Sulfation.
 FT PEPTIDE 1 19 FIBRINOPEPTIDE B.
 FT MOD_RES 3 3 SULFATION.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA: 2296 MW: 921A2B02D5F6891D CRC64;
 Query Match 15.8%; Score 3; DB 1; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 11 GRT 13
 DB 10 GRT 12
 RESULT 17
 MTFH_TRIMR STANDARD; PRT; 19 AA.
 AC P81530;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE L-dopachrome-methyl ester tautomerase (macrophage migration inhibitory
 DE factor homolog) (Fragment).
 OS Trichuris muris.
 CC Eukaryota; Metazoa; Nematoda; Enophea; Trichocephalida; Trichuridae;
 CC Trichuris.
 OX NCBI_TaxID=70415;
 RN (1)
 RP SEQUENCE.
 RC MEDLINE=99013685; PubMed=9794786;
 RA Pennock J.L., Behnke J.M., Blackie O.D., Devaney E., Grencis R.K.,
 RA Isaac R.E., Joshua G.W.P., Selkirk M.E., Zhang Y., Meyer D.J.;
 RT "Rapid purification and characterization of L-dopamine-methyl-ester
 RT tautomerase (macrophage migration inhibitory factor) from Trichinella
 RT spiralis, Trichuris muris and Brugia pahangi.";
 RL Biochem. J. 335:495-498(1998).
 CC -i- FUNCTION: TAUTOMERIZATION OF THE METHYL ESTER OF L-DOPACHROME.
 CC -i- SIMILARITY: INHIBITED BY FREE FATTY ACIDS AND HEMATIN.
 DR InterPro: IPR001398; MTF.
 DR PROSITE: PS01158; MTF; PARTIAL.
 KW Cytokine.

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FT NON_TER 19 19
SQ SEQUENCE 19 AA: 2058 MW: F7D70C81D12F1234 CRC64:

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 19;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NVP 3
    |||
Db 8 NVP 10

RESULT 18
ALAT_PIG STANDARD; PRT; 20 AA.
AC P13191.
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
P1 Alaline aminotransferase (EC 2.6.1.2) (Glutamic--pyruvic transaminase)
GN (GPT) (Glutamic--alanine transaminase) (Fragment).
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN NCBI_TaxID=9823;
RP [1]
RT SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=79232426; PubMed=465450;
RT Tanase S., Kojima H., Morino Y.;
RT "Pyridoxal 5'-phosphate binding site of pig heart alaline
RT aminotransferase."
RL Biochemistry 18:3002-3007(1979).
CC -1- FUNCTION: PARTICIPATES IN CELLULAR NITROGEN METABOLISM AND ALSO
CC IN LIVER GLUCONEGENESIS STARTING WITH PRECURSORS TRANSPORTED
CC FROM SKELETAL MUSCLES.
CC -1- CATALYTIC ACTIVITY: L-alanine + 2-oxoglutarate = pyruvate + L-
CC glutamate.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- MISCELLANEOUS: THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A
CC MITOCHONDRIAL ONE.
CC -1- SIMILARITY: TO OTHER SPECIES ALANINE AMINOTRANSFERASE.
DR PIR: A14344; A14344.
KM Transferase; Aminotransferase; Pyridoxal phosphate.
RN NON_TER 1 1
P1 BINDING 11 11 PYRIDOXAL PHOSPHATE.
P1 NON_TER 20 20
SQ SEQUENCE 20 AA: 2217 MW: 1C2243A373EC4801 CRC64:

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ELA 19
    |||
Db 2 ELA 4

RESULT 19
EFTU_MYCSY STANDARD; PRT; 20 AA.
AC P81407.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Elongation factor Tu (Ef-Tu) (Fragment).
GN TUF.
OS Mycoplasma synoviae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2109;

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RN [1]
RP SEQUENCE.
RC STRAIN=UBB 925 / Isolate KP9;
RX MEDLINE=99237234; PubMed=10220885;
RA Bencina D., Narat M., Dovic P., Drobnic-Valic M., Habe F., Kleven S.H.;
RT "The characterization of Mycoplasma synoviae EF-Tu protein and
RT proteins involved in hemadherence and their N-terminal amino acid
RT sequences."
RL FEMS Microbiol. Lett. 173:85-94(1999).
CC -1- FUNCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT BINDING OF
CC AMINOACYL-tRNA TO THE A-SITE OF RIBOSOMES DURING PROTEIN
CC BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC EF-TU/EF-1A SUBFAMILY.
DR InterPro: IPR000795; EF_GTPbind
DR PROSITE: PS00301; EFACOR_GTP; PARTIAL.
KW Elongation factor; Protein biosynthesis; GTP-binding.
P1 NON_TER 20 20
SQ SEQUENCE 20 AA: 2222 MW: C3C92564B740ACC6 CRC64:

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Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 SKE 17
    |||
Db 8 SKE 10

RESULT 20
ITRA_ALBUJ STANDARD; PRT; 20 AA.
ID P24925.
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Trypsin inhibitor A chain (Fragment).
DE Albizzia julibrissin (Silk tree).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Mimosoideae; Ingeae; Albizzia.
OX NCBI_TaxID=3813;
RN [1]
RP SEQUENCE.
RC TISSUE=Seed;
RX MEDLINE=80115605; PubMed=528539;
RA Odani S., Ono T., Ikenaka T.;
RT "Proteinase inhibitors from a mimosoideae legume, Albizzia
RT julibrissin. Homologues of soybean trypsin inhibitor (Kunitz).";
RL J. Biochem. 86:1795-1805(1979).
CC -1- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
CC -1- SUBUNIT: HETERODIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -1- SIMILARITY: BELONGS TO THE LEGUMINOUS KUNITZ-TYPE INHIBITOR
CC FAMILY.
DR InterPro: IPR002160; Kunitz_legume.
DR Pfam: PF00197; Kunitz_legume; 1.
DR PROSITE: PS00283; SOYBEAN_KUNITZ; 1.
KM Serine protease inhibitor.
P1 NON_TER 20 20
SQ SEQUENCE 20 AA: 2191 MW: 143737629377C25 CRC64:

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Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 KEL 18
    |||
Db 1 KEL 3

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RESULT 21
LYC_FELCA          STANDARD:          PRT:          20 AA.
ID   LYC_FELCA
AC   P37155
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DE   15-0UN-2002 (Rel. 41, Last annotation update)
DE   Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C) (Fragment).
GN   Lyz.
OS   Fells silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Fells.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE.
RC   TISSUE= Milk;
RX   MEDLINE=90263403; PubMed=2344734;
RT   Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.;
RT   "Feline whey proteins: Identification, isolation and initial
RT   characterization of alpha-lactalbumin, beta-lactoglobulin and
RT   lysozyme.";
CC   Comp. Biochem. Physiol. 95B:773-779(1990).
CC   -1- FUNCTION: Lysozymes have primarily a bacteriolytic function: those
CC   in tissues and body fluids are associated with the monocyte-
CC   macrophage system and enhance the activity of immunoenzymes.
CC   -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
CC   acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
CC   heteropolymers of the prokaryotes cell walls.
CC   -1- SUBUNIT: MONOMER.
CC   -1- MISCELLANEOUS: Lysozyme C is capable of both hydrolysis and
CC   transglycosylation. It shows also a slight esterase activity. It
CC   acts rapidly on both peptide-substituted and unsubstituted
CC   peptidoglycan, and slowly on chitin oligosaccharides.
CC   -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
DR   PIR: A60525; A60525.
DR   HSSP: P11376; 2B0L.
DR   InterPro: IPR001916; GH_22.
DR   Pfam: PF00062; lys_1.
DR   PROSITE: PS00128; LACTALBUMIN_LYSOZYME; PARTIAL.
RT   Hydrolyase; Glycosidase; Bacteriolytic enzyme; Milk.
FT   NON_TER
SQ   SEQUENCE 20 AA; 2314 MW; EB8824EA59425F13 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 ELA 19
    |||
    7 ELA 9

RESULT 22
MIF_PIG          STANDARD:          PRT:          20 AA.
ID   MIF_PIG
AC   P80928
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Macrophage migration inhibitory factor (MIF) (Phenylpyruvate
DE   tautomerase) (Glycosylation-inhibiting factor) (GIF) (Fragment).
GN   MIF.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RC   Riviere S., Bouet F., Menez A., Galat A.;
RX   Submitted (MAR-1997) to the SWISS-PROT data bank.
RT   -1- FUNCTION: THE EXPRESSION OF MIF AT SITES OF INFLAMMATION SUGGEST A
RT   ROLE FOR THE MEDIATOR IN REGULATING THE FUNCTION OF MACROPHAGE IN
RT   HOST DEFENSE. ALSO ACTS AS A PHENYLPIRUVATE TAUTOMERASE (BY

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CC   SIMILARITY).
CC   -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC   -1- SIMILARITY: BELONGS TO THE MIF FAMILY.
DR   HSSP: P14174; 1GIF.
DR   InterPro: IPR001398; MIF.
DR   Pfam: PF01187; MIF_1.
DR   PROSITE: PS01158; MIF; PARTIAL.
KW   Isomerase; Macrophage; Inflammatory response; Cytokine.
FT   ACT_SITE 1
FT   NON_TER 20
SQ   SEQUENCE 20 AA; 2147 MW; 3517AF60F3012A61 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NVP 3
    |||
    8 NVP 10

RESULT 23
PORC_METTM      STANDARD:          PRT:          20 AA.
ID   PORC_METTM
AC   P80902;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Pyruvate synthase subunit PORC (EC 1.2.7.1) (Pyruvate oxidoreductase
DE   gamma chain) (POR) (Pyruvic-ferredoxin oxidoreductase gamma subunit)
DE   (Fragment).
GN   PORC.
OS   Methanobacterium thermoautotrophicum (strain Marburg / DSM 2133).
OC   Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC   Methanobacteriaceae; Methanothermobacter.
OX   NCBI_TaxID=79929;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=97261844; PubMed=9108258;
RT   Terreegeen A., Linder D., Thauer R.K., Hedderich R.;
RT   "Structures and functions of four anaerobic 2-oxoacid oxidoreductases
RT   in Methanobacterium thermoautotrophicum.";
RL   Eur. J. Biochem. 244:862-868(1997).
CC   -1- FUNCTION: THE PH OPTIMUM IS PH 10.0 AND THE OPTIMAL TEMPERATURE
CC   IS 80 DEGREES CELSIUS.
CC   -1- CATALYTIC ACTIVITY: Pyruvate + CoA + oxidized ferredoxin = acetyl-
CC   CoA + CO(2) + reduced ferredoxin.
CC   -1- COFACTOR: BINDS TWO 4Fe-4S CLUSTERS (BY SIMILARITY).
CC   -1- SUBUNIT: HETEROTETRAMER OF ONE ALPHA, ONE BETA, ONE DELTA AND ONE
CC   GAMMA CHAIN.
CC   -1- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
KW   Oxidoreductase; Electron transport; Iron-sulfur; Repeat; 4Fe-4S.
FT   NON_TER 20
SQ   SEQUENCE 20 AA; 2167 MW; 481532134D42F353 CRC64;

Query Match
Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 GRG 11
    |||
    8 GRG 10

RESULT 24
PSBM_WHEAT      STANDARD:          PRT:          20 AA.
ID   PSBM_WHEAT
AC   P55967;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Photosystem II reaction center w protein (PSII 6.1 kDa protein)
DE   (Fragment).

```


Search completed: May 9, 2003, 16:05:45
 Job time : 12 secs

GN PSM.
 OS Trifolium aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
 OC Triliceae; Trilicium.
 OX NCBI_TaxID=4565;
 RN (1)
 RP SEQUENCE.

RX MEDLINE=89121082; PubMed=2644131;
 RA Ikeuchi M., Takio K., Inoue Y.;

RT "N-terminal sequencing of photosystem II low-molecular-mass proteins.
 S and 4.1 kDa components of the O₂-evolving core complex from higher
 plants.";

RL FEBS Lett. 242:263-269(1989).
 CC -1- FUNCTION: SUBUNIT OF THE WATER OXIDATION COMPLEX OF PHOTOSYSTEM II
 CC REACTION CENTER COMPLEX.

CC -1- SIMILARITY: BELONGS TO THE PSM FAMILY.
 KM Photosynthesis; Photosystem II; Thylakoid; Membrane; Chloroplast.

FT NON_TER 20 20
 SEQUENCE 20 AA; 2093 MW; E26468763375B5C9 CRC64;

Query Match

Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 ERM 8
 111
 Db 4 ERM 6

RESULT 25

RIPX_CUCPE STANDARD; PRT; 20 AA.

ID RIPX_CUCPE

AC P80750;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Ribosome-inactivating protein (RNA N-glycosidase) (EC 3.2.2.22)

DE (Fragment).

OS Cucurbita pepo (Vegetable marrow) (Summer squash).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eucotsids I; Cucurbitales; Cucurbitaceae; Cucurbita.

OX NCBI_TaxID=3663;

RN (1)

RP SEQUENCE.

RC TISSUE=Mesocarp;

MEDLINE=97175025; PubMed=9022685;

Yoshinari S., Yokota S., Sawamoto H., Koresawa S., Tamura M.,

Endo Y.;

"Purification, characterization and subcellular localization of a
 type-1 ribosome-inactivating protein from the sarcocarp of Cucurbita
 pepo.";

Eur. J. Biochem. 242:585-591(1996).

-1- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
 specific adenosine on the 28S rRNA.

-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
 TYPE 1 RIP SUBFAMILY.
 InterPro: IPR001574; RIP.
 DR Pfam: PF00161; RIP; 1.
 DR PROSITE: PS00275; SHIGA_RICIN; PARTIAL.
 KM Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin.
 FT NON_TER 20 20
 SEQUENCE 20 AA; 2235 MW; 8E753D217FDEA6D CRC64;

Query Match

Best Local Similarity 15.8%; Score 3; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TSS 15
 111
 Db 10 TSS 12

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 9, 2003, 15:39:19 ; Search time 34 Seconds
(without alignments)
74.464 Million cell updates/sec

Title: US-09-674-913a-1

Perfect score: 19
Sequence: 1 NVPGERMGRRTSKELA 19

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Size: 0

Total number of hits satisfying chosen parameters: 158699

Minimum DB seq length: 10
Maximum DB seq length: 20

Post-processing: listing first 45 summaries

Database: A Geneseq.101002.*

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19: /SID52/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SID52/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SID52/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	19	AA56391	Mutant beta-APP pr
2	15	78.9	19	AA56391	AMY6 peptide. Uni
3	13	68.4	14	AA56391	AMY5 peptide. Uni
4	12	63.2	12	AA56391	Mutant beta-APP pr
5	10	52.6	10	AA56391	Peptide resulting
6	10	52.6	10	AA56391	Human beta-APP imm
7	10	52.6	10	AA56391	AMY1 peptide. Uni
8	9	47.4	17	AA56391	Mutant beta-APP pr
9	8	42.1	15	AA56391	Mutant ubiquitin-B
10	5	26.3	10	AA56391	Tumour antigen pro

11	5	26.3	10	AA56391	Saccharomyces cere
12	5	26.3	10	AA56391	Saccharomyces cere
13	5	26.3	10	AA56391	Saccharomyces cere
14	5	26.3	10	AA56391	Human peptide #150
15	5	26.3	15	AA56391	G2 peptide. Unide
16	5	26.3	18	AA56391	Hypothetical signa
17	5	26.3	19	AA56391	hmf1 Mitofusin GT
18	4	21.1	10	AA56391	IL-6 antagonist pe
19	4	21.1	10	AA56391	Hepatitis C virus
20	4	21.1	10	AA56391	Hepatitis C virus
21	4	21.1	10	AA56391	Hydroxymethylgluta
22	4	21.1	10	AA56391	SH2 binding peptid
23	4	21.1	10	AA56391	CD34 antigen anti
24	4	21.1	10	AA56391	scfv 9A4 clone 23A
25	4	21.1	10	AA56391	Chemokine peptide,
26	4	21.1	10	AA56391	Human chemokine GR
27	4	21.1	10	AA56391	EMCV 3C protease u
28	4	21.1	10	AA56391	Claudin-2 cyclic c
29	4	21.1	10	AA56391	Claudin-2 cyclic c
30	4	21.1	10	AA56391	Claudin-2 cyclic c
31	4	21.1	10	AA56391	Claudin-2 cyclic c
32	4	21.1	10	AA56391	Claudin-2 cyclic c
33	4	21.1	10	AA56391	Claudin-2 cyclic c
34	4	21.1	10	AA56391	Claudin-2 cyclic c
35	4	21.1	10	AA56391	Streptavidin displ
36	4	21.1	10	AA56391	Human haematopoiet
37	4	21.1	10	AA56391	HIV A1 motif gag
38	4	21.1	10	AA56391	Monoclonal antibod
39	4	21.1	10	AA56391	Mycoplasma genital
40	4	21.1	10	AA56391	Human complementar
41	4	21.1	10	AA56391	Human complementar
42	4	21.1	10	AA56391	Human complementar
43	4	21.1	10	AA56391	Human complementar
44	4	21.1	10	AA56391	Human complementar
45	4	21.1	10	AA56391	Human complementar

ALIGNMENTS

RESULT 1
AA56391
ID AA56391 standard; peptide; 19 AA.
AC AA56391;
XX
DT 15-FEB-2000 (first entry)
XX
DE Mutant beta-APP protein peptide sequence SEQ ID NO:1.
XX
KW Mutant; beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
KW gene therapy.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9358564-A1.
XX
PD 18-NOV-1999.
XX
PF 30-APR-1999; 99WO-NO00141.
XX
PR 08-MAY-1998; 98NO-0002096.
XX
PA (NHYD) NORSK HYDRO AS.
XX
PI Gaudernack G, Eriksen JA, Moller M;
XX WPI: 2000-039070/03.
XX
PT Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
useful for treating Alzheimer's disease and Down syndrome

XX
PS Claim 10; Page 27; 33pp; English.

The present invention describes frameshift mutant beta-amyloid precursor peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B (Ubi-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and Down syndrome eliciting T cellular immunity. The peptides may be used as a vaccine for Alzheimer's disease and Down syndrome. The vaccination is sufficient to induce specific T-cell immunity to mutant beta-APP and/or Ubi-B peptides that are associated with Alzheimer's disease or Down syndrome. The patient may be stimulated in vivo or ex vivo with the peptides. The peptides and DNA encoding the peptides can also be used for the treatment or prophylaxis of Alzheimer's disease or the treatment of Down syndrome.

Sequence 19 AA;

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Query match 100.0%; Score 19; DB 21; Length 19;
```

Best Local Similarity 100.0%; Pred. No. 6,4e-13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 NVRGHERMGRGRTSSKELA 19

RESULT 2
AAB99216

AAC 992167

DT 06-SEP-2001 (first entry)

AMY6 peptide.

KM AM6; disease detection; age-related disease; Alzheimer's disease;
KM Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KM amyotrophic lateral sclerosis; Huntington's disease;
KM spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
KM degenerative disease; cardiovascular disease; rheumatoid arthritis;
KM beta-amyloid precursor protein; APP.

Unidentified OS

PN WO200140804-A2

07-JUN-2001

04-DEC-2000; 2000WO-NL008887.

PR 03-DEC-1999; 99EP-0204140.

PA (NEVV-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE

PI HOL EM, Van Leeuwen FW;

DR WPI; 2001-397965/42.

AA Detecting a disease or pathological condition, associated with
 PT secretion of aberrant protein e.g. age-related diseases, by determining
 PT level of aberrant protein and/or its detectable part in body fluid
 PT and/or tissue -

PS Disclosure; Page 24; 36pp; English

CC The present invention relates to a method for detecting a disease or
CC pathological condition associated with molecular misreading of coding
CC sequences in the genome and/or associated with the clearance of aberrant
CC protein. The method comprises providing a sample of a body fluid and/or
CC tissue of a patient and determining a level of the aberrant protein
CC and/or its detectable part or the ratio between the two in the body fluid
CC and/or tissue. The method enables diagnosing the disease before the

CC patient exhibits clinical symptoms. The method is useful for diagnosing
CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or
CC other age related diseases e.g. cancer, neurodegenerative diseases, such
CC as frontal lobe dementia, progressive supranuclear palsy; and other
CC diseases with abundant tau-positive filamentous lesions, Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease,
CC spinocerebellar ataxia-3, multiple sclerosis, Huntington's disease,
CC diseases associated with ubiquitin, diabetes mellitus type II and other
CC degenerative diseases such as cardiovascular diseases and rheumatoid
CC arthritis. A number of other diseases which can be diagnosed are given in
CC the specification. The present sequence is AMY 6 peptide, which was
CC coupled to thyroglobulin by glutaraldehyde, and used to immunise
CC rabbits for antibody production in the present invention. The AMY 6
CC peptide is a C-terminal fragment of the full-length beta-amyloid
CC precursor protein (APP-1; mature APP and its signal peptide) protein.

Sequence 19 AA:

Query Match	Score	DB	Length
78.9%	15	22	19

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Best Local Similarity 100.0%; Pred. No. 8.5e-09,
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 5 HERMGRGRTSSKELA 19

RESULT 3
AAB99215
ID AAB99215 standard; peptide; 14 AA

AC AAB99215;

DT 06-SEP-2001 (first entry)

DE AMY5 peptide.

KW AMY5, disease detection, age-related disease; Alzheimer's disease;
KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
KW amyotrophic lateral sclerosis; Huntington's disease;
KW spinocerebellar ataxia-7; multiple sclerosis; diabetes mellitus type II;
KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
KW beta-amyloid precursor protein; APP.

Unidentified OS

PN W0200140804-A2

PD 07-JUN-2001

PF 04-DEC-2000; 2000WO-NL00887.

PR 03-DEC-1999; 99EP-0204140.

PA (NEUW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE

PI HOL EM, Van Leeuwen FW;

DR WPI; 2001-397965/42.

aa Detecting a disease or pathological condition, associated with
 PT secretion of aberrant protein e.g. age-related diseases, by determining
 PT level of aberrant protein and/or its detectable part in body fluid
 PT and/or tissue -

PS Disclosure; page 24; 36pp; English

AA The present invention relates to a method for detecting a disease or
CC pathological condition associated with molecular misreading of coding
CC sequences in the genome and/or associated with the clearance of aberrant
CC protein. The method comprises providing a sample of a body fluid and/or
CC tissue of a patient and determining a level of the aberrant protein
CC and/or its detectable part or the ratio between the two in the body fluid

CC and/or tissue. The method enables diagnosing the disease before the
CC patient exhibits clinical symptoms. The method is useful for diagnosing
CC age-related diseases, preferably Alzheimer's disease, Down's syndrome or
CC other age related diseases e.g. cancer; neurodegenerative diseases, such
CC as frontal lobe dementia, progressive supranuclear palsy; and other
CC diseases with abundant tau-positive, filamentous lesions; Parkinson's
CC disease, amyotrophic lateral sclerosis, Huntington's disease,
CC spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
CC diseases associated with ubiquitin, diabetes mellitus type II and other
CC degenerative diseases such as cardiovascular diseases and rheumatoid
CC arthritis. A number of other diseases which can be diagnosed are given in
CC the specification. The present sequence is AMY 5 peptide, which was
CC coupled to thyroglobulin by glutaraldehyde, and used to immunise
CC rabbits for antibody production in the present invention. The AMY 5
CC peptide is a C-terminal fragment of the full-length beta-amyloid
CC precursor protein (APP+1; mature APP and its signal peptide) protein.
XX
XX
SQ Sequence 14 AA:

Query Match 68.4%; Score 13; DB 22; Length 14;
Best Local Similarity 100.0%; Pred. No. 7.6e-07;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 RMGRGRTSSKELA 19
|||||
DB 2 RMGRGRTSSKELA 14

RESULT 4
ID AAY56394 standard; peptide; 12 AA.
XX
XX AAY56394;

XX 15-FEB-2000 (first entry)

XX Mutant beta-APP protein peptide sequence SEQ ID NO:4.

XX Mutant: beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KW Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
gene therapy.

XX Synthetic.
OS Homo sapiens.

XX MO9958564-A1.

XX 18-NOV-1999.

XX 30-APR-1999; 99MO-NO00141.

XX 08-MAY-1998; 98NO-0002098.

XX (NHMD) NORSK HYDRO AS.

XX Gaudernack G, Eriksen JA, Moller M;

XX WPI; 2000-039070/03.

XX Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
XX useful for treating Alzheimer's disease and Down syndrome
XX Claim 10; Page 27; 33pp; English.

XX The present invention describes frameshift mutant beta-amyloid precursor
XX peptides (beta-APP) (AAY56394) and mutant ubiquitin-B
XX (ubi-B) (AAY56400) associated with Alzheimer's disease and
XX Down syndrome eliciting T cellular immunity. The peptides may be used as
XX a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
XX sufficient to induce specific T-cell immunity to mutant beta-APP and/or
XX ubi-B peptides that are associated with Alzheimer's disease or Down
XX syndrome. The patient may be stimulated in vivo or ex vivo with the
XX peptides. The peptides and DNA encoding the peptides can also be used for

CC the treatment or prophylaxis of Alzheimer's disease or the treatment of
CC Down syndrome.

SQ Sequence 12 AA:

Query Match 63.2%; Score 12; DB 21; Length 12;
Best Local Similarity 100.0%; Pred. No. 7.2e-06;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 MGRGRTSSKELA 19
|||||
DB 1 MGRGRTSSKELA 12

RESULT 5
ID AAM18633 standard; peptide; 10 AA.
XX
XX AAM18633;

XX 21-JUL-1997 (first entry)

XX Peptide resulting from human amyloid A4 gene +1 frameshift mutation.

XX Frameshift mutation product; GAGA motif; somatic mutation; diagnosis;
XX detection; antibody; probe; cancer; neoplasia; neurodegenerative;
XX Parkinson's; Alzheimer's disease; Pick's; Huntington's disease;
XX Down's syndrome; frontal lobe dementia; progressive supranuclear palsy;
XX PSP; amyotrophic lateral sclerosis; multiple sclerosis; MS;
XX cardiovascular; rheumatoid arthritis.

XX Homo sapiens.

XX MO9712992-A2.

XX 10-APR-1997.

XX 02-OCT-1996; 96MO-IB01106.

XX 11-JAN-1996; 96US-0009832.

XX 02-OCT-1995; 95GB-0020080.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
XX (UYRO-) UNIV ROTTERDAM ERASMUS.
XX (UYUT-) UNIV STATE UTRECHT.

XX Burbach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI; 1997-226235/20.

XX Use of mutant genes having frame:shift mutation(s) - for developing
XX prods. for the diagnosis, prevention and treatment of associated
XX diseases, e.g. cancer or neurodegenerative disease

XX Claim 24; Page 82; 123pp; English.

XX AAM18633-WI8641 are antigenic peptide products of +1 and +2 frameshift
XX mutations of various human genes including the amyloid A4, tau,
XX ubiquitin, apolipoprotein E, microtubule-associated protein 2,
XX (MAP-2) and neurofilament subunit L, M and H genes. The peptides
XX are used for the production of antibodies which can be used in the
XX diagnosis, prevention and treatment of diseases such as cancer or
XX neurodegenerative disease, e.g. Parkinson's disease, Alzheimer's
XX Down's syndrome, frontal lobe dementia (Pick's disease), progressive
XX supranuclear palsy (PSP), amyotrophic lateral sclerosis, Huntington's
XX disease, multiple sclerosis, and other degenerative diseases such as
XX cardiovascular diseases and rheumatoid arthritis.

SQ Sequence 10 AA:
Query Match 52.6%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19
 |||||
 1 RGRSSKELA 10

RESULT 6
 AAY20152
 ID AAY20152 standard; Peptide: 10 AA.

XX AAY20152;

XX 22-JUL-1999 (first entry)

DE Human beta-APP immunogenic peptide fragment.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis: cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;
 KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW Huntington's disease; multiple sclerosis associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A;
 KW immunogenic.

XX Homo sapiens.

XX MO9845322-A2.

XX 15-OCT-1998.

XX 02-APR-1998; 98WO-IB00705.

XX 10-APR-1997; 97US-0043163.

XX (UYUT-) RIJKSUNIV UTRECHT.

XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.

XX (UYRO-) UNIV ROTTERDAM ERASMUS.

XX Burchach JPH, Grosveld FG, Van Leeuwen FW;

XX WPI: 1998-609901/51.

XX Diagnosing disease by detecting frameshift mutations in RNA or
 XX corresponding protein mutations - used to diagnose cancer and
 XX neurological diseases, particularly Alzheimer's disease, and also
 XX for treatment and prevention with specific ribozymes or wild-type
 XX RNA

XX Claim 24; Page 85; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease
 XX caused by, or associated with, an RNA molecule that has a frameshift
 XX mutation. The method is used to diagnose age-related diseases, especially
 XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 XX and many others listed) or susceptibility to these disorders. The method
 XX allows a definitive diagnosis of Alzheimer's disease in living patients,
 XX at an early stage. It is based on the observation that disease may be
 XX caused by mutations in RNA rather than DNA. The invention describes the
 XX use of neuronal system RNA molecules, specifically proteins including
 XX beta-amyloid precursor protein (beta-APP), the microtubule associated
 XX proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 XX 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 XX protein-C (HMGP-C) and neuroendocrine specific protein A.

SQ Sequence 10 AA:

Query Match 52.6%; Score 10; DB 19; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.00072;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 RGRSSKELA 19
 |||||
 Db 1 RGRSSKELA 10

RESULT 7
 AAB99214

ID AAB99214 standard; peptide: 10 AA.

XX AAB99214;

XX 06-SEP-2001 (first entry)

DE AMY1 peptide.

XX AMY1; disease detection; age-related disease; Alzheimer's disease;
 KW Down's syndrome; cancer; neurodegenerative disease; Parkinson's disease;
 KW amyotrophic lateral sclerosis; Huntington's disease;
 KW spinocerebellar ataxia-3; multiple sclerosis; diabetes mellitus type II;
 KW degenerative disease; cardiovascular disease; rheumatoid arthritis;
 KW beta-amyloid precursor protein; APP.

XX Unidentified.

XX WO200140804-A2.

XX 07-JUN-2001.

XX 04-DEC-2000; 2000WO-NL00887.

XX 03-DEC-1999; 99EP-0204140.

XX (NEUW-) KONINK NEDERLANDSE AKAD VAN WETENSCHAPPE.

XX HOL EM, Van Leeuwen FW;

XX WPI: 2001-397965/42.

XX Detecting a disease or pathological condition, associated with
 XX secretion of aberrant protein e.g. age-related diseases, by determining
 XX level of aberrant protein and/or its detectable part in body fluid
 XX and/or tissue

XX Disclosure: Page 24; 36pp; English.

XX The present invention relates to a method for detecting a disease or
 XX pathological condition associated with molecular misreading of coding
 XX sequences in the genome and/or associated with the clearance of aberrant
 XX protein. The method comprises providing a sample of a body fluid and/or
 XX tissue of a patient and determining a level of the aberrant protein
 XX and/or its detectable part or the ratio between the two in the body fluid
 XX and/or tissue. The method enables diagnosing the disease before the
 XX patient exhibits clinical symptoms. The method is useful for diagnosing
 XX age-related diseases, preferably Alzheimer's disease, Down's syndrome or
 XX other age related diseases e.g. cancer; neurodegenerative diseases, such
 XX as frontal lobe dementia, progressive supranuclear palsy; and other
 XX diseases with abundant tau positive filamentous lesions, Parkinson's
 XX disease, amyotrophic lateral sclerosis, Huntington's disease,
 XX spinocerebellar ataxia-3, multiple sclerosis; other inclusion body
 XX diseases associated with ubiquitin, diabetes mellitus type II and other
 XX degenerative diseases such as cardiovascular diseases and rheumatoid
 XX arthritis. A number of other diseases which can be diagnosed are given in
 XX the specification. The present sequence is AMY 1 peptide, which was
 XX coupled to thyroglobulin by glutaraldehyde, and used to immunise
 XX rabbits for antibody production in the present invention. The AMY 1
 XX peptide is a C-terminal fragment of the full-length beta-amyloid
 XX precursor protein (APP+1; mature APP and its signal peptide) protein.

[illegible]

ID	AAV56395 standard; peptide: 15 AA.
XX	
AC	AAV56395;
XX	
DT	15-FEB-2000 (first entry)
XX	
DE	Mutant ubiquitin-B peptide sequence SEQ ID NO:5.
XX	
KW	Mutant: beta-amyloid precursor protein; beta-APP; ubiquitin-B; vaccine;
KM	Alzheimer's disease; Down syndrome; T cellular immunity; neuroprotective;
OS	gene therapy.
XX	
OS	Synthetic.
XX	Homo sapiens.
PN	MO9958564-A1.
PD	18-NOV-1999.
XX	
PF	30-APR-1999; 99WO-N000141.
XX	
PR	08-MAY-1998; 98NO-0002098.
PA	(NH ₂ D) NORSK HYDRO AS.
PI	Gaudernack G, Eriksen JA, Møller M;
DR	WPI; 2000-039070/03.
PT	Frameshift mutant beta-amyloid precursor and ubiquitin-B peptides,
XX	useful for treating Alzheimer's disease and Down syndrome
PS	Claim 10; Page 27; 33pp; English.
XX	
CC	The present invention describes frameshift mutant beta-amyloid precursor
CC	peptides (beta-APP) (AAV56391 to AAV56394) and mutant ubiquitin-B
CC	(Ubi-B) (AAV56395 to AAV56400) associated with Alzheimer's disease and
CC	Down syndrome eliciting T cellular immunity. The peptides may be used as
CC	a vaccine for Alzheimer's disease and Down syndrome. The vaccination is
CC	sufficient to induce specific T-cell immunity to mutant beta-APP and/or
CC	Ubi-B peptides that are associated with Alzheimer's disease or Down
CC	syndrome. The patient may be stimulated in vivo or ex vivo with the
CC	peptides. The peptides and DNA encoding the peptides can also be used for
CC	the treatment or prophylaxis of Alzheimer's disease or the treatment of
XX	Down syndrome.
XX	
SQ	Sequence 15 AA;
XX	
Query Match	42.1%; Score 8; DB 21; Length 15;
Best Local Similarity	100.0%; Pred. No. 0.12;
Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	7 RMGRGRTS 14
DB	
	8 RMGRGRTS 15
RESULT 10	
ID	AAV85440
XX	AAV85440 standard; peptide: 10 AA.
AC	AAV85440;
XX	
DT	23-JUN-2000 (first entry)
DE	Tumour antigen protein SART-3 peptide derivative #20.
XX	
KM	Tumour antigen protein; SART-3; cytotoxic T-cell; HLA antigen; tumour.
OS	Homo sapiens.
XX	
PN	WO200012701-A1.
XX	

PD 09-MAR-2000.
XX 27-AUG-1999; 99WO-JP04622.
XX 28-AUG-1998; 98JP-0242660.
XX (SUMU) SUMITOMO PHARM CO LTD.
PA (ITOH/) ITOH K.
XX Itoh K, Nakao M;
PI WPI: 2000-237868/20.
DR Tumor antigen protein SART-3 recognized by cytotoxic T-cells binding to
PT HLA antigen for treatment and diagnosis of tumors -
XX Claim 11: Page 68; 89pp; Japanese.
PS The invention provides a tumour antigen protein (SART-3) which is
CC recognized by cytotoxic T-cells binding to HLA antigen. SART-3 can be
C expressed by standard recombinant methodology. SART-3 and its peptide
CC derivatives can be used in the prevention, treatment and diagnosis of
CC tumours in vitro or in vivo. Sequences AAT85423-484 represent peptide
CC derivatives of SART-3.
XX
SQ Sequence 10 AA;
Query Match 26.3%; Score 5; DB 21; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 14 SSKEL 18
DB 6 SSKEL 10
RESULT 11
AAG85559
ID AAG85559 standard; Peptide; 10 AA.
XX AAG85559;
AC
XX 11-SEP-2001 (first entry)
DT
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 508.
DE
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
C
XX Saccharomyces cerevisiae.
C
XX WO200142276-A1.
PN
XX 14-JUN-2001.
PD
XX 13-DEC-2000; 2000WO-GB04773.
PF
XX 13-DEC-1999; 99GB-0029471.
PR
XX (PROT-) PROTEOM LTD.
PA
XX Roberts GW, Heal JR;
PI WPI: 2001-367863/38.
DR
XX Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX Example 3; Page 100; 488pp; English.
PS The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC euakaryotic genomes, excluding human and plants. The specific

CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
XX
SQ Sequence 10 AA;
Query Match 26.3%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GRGRT 13
DB 6 GRGRT 10
RESULT 12
AAG85565
ID AAG85565 standard; Peptide; 10 AA.
XX AAG85565;
AC
XX 11-SEP-2001 (first entry)
DT
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 514.
DE
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
KW drug discovery; drug design.
C
XX Saccharomyces cerevisiae.
C
XX WO200142276-A1.
PN
XX 14-JUN-2001.
PD
XX 13-DEC-2000; 2000WO-GB04773.
PF
XX 13-DEC-1999; 99GB-0029471.
PR
XX (PROT-) PROTEOM LTD.
PA
XX Roberts GW, Heal JR;
PI WPI: 2001-367863/38.
DR
XX Identifying complementary peptides by analysis of protein and
PT nucleotide sequence databases, useful in drug design -
XX Example 3; Page 100; 488pp; English.
PS The invention relates to the identification of complementary peptides
CC by analysis of protein and nucleotide sequence databases from higher
CC eukaryotic genomes, excluding human and plants. The specific
CC complementary peptides interact with their relevant target proteins
CC encoded in the eukaryote genome. The peptides may be used as reagents
CC and drugs for drug discovery and as lead ligands for drug design and
CC development. The present sequence is a complementary peptide from
CC Saccharomyces cerevisiae.
C
XX Sequence 10 AA;
Query Match 26.3%; Score 5; DB 22; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GRGRT 13
DB 6 GRGRT 10
RESULT 13
AAG85579

ID AAG85579 standard; Peptide: 10 AA.
 XX AAG85579;
 AC
 XX
 XX
 DT 11-SEP-2001 (first entry)
 XX
 XX Saccharomyces cerevisiae peptide; SEQ ID NO: 528.
 DE
 XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
 XX drug discovery; drug design.
 KW
 XX Saccharomyces cerevisiae.
 OS
 XX WO200142276-A1.
 XX
 XX 14-JUN-2001.
 PD
 XX 13-DEC-2000; 2000WO-GB04773.
 XX
 XX 13-DEC-1999; 99GB-0023471.
 XX
 XX (PROT-) PROTEOM LTD.
 XX
 XX Roberts GW, Heal JR;
 PI
 XX WPI: 2001-367863/38.
 DR
 XX
 XX
 XX Identifying complementary peptides by analysis of protein and
 PT nucleotide sequence databases, useful in drug design -
 XX
 XX Example 3; Page 102; 488pp; English.
 PS
 XX The invention relates to the identification of complementary peptides
 CC by analysis of protein and nucleotide sequence databases from higher
 CC eukaryotic genomes, excluding human and plants. The specific
 CC complementary peptides interact with their relevant target proteins
 CC encoded in the eukaryote genome. The peptides may be used as reagents
 CC and drugs for drug discovery and as lead ligands for drug design and
 CC development. The present sequence is a complementary peptide from
 CC Saccharomyces cerevisiae.
 CC
 SQ Sequence 10 AA;
 Query Match 26.3%; Score 5; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 9 GRCRT 13
 6 GRCRT 10
 RESULT 14
 AAM98228
 ID AAM98228 standard; Peptide: 14 AA.
 XX
 AC AAM98228;
 XX
 XX 24-JAN-2002 (first entry)
 DT
 XX Human peptide #1503 encoded by a SNP oligonucleotide.
 DE
 XX
 XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
 KW neuroprotective; antitubercular; gene therapy; vaccine; amylose; cancer;
 KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
 KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
 KW complement related protein; cytochrome; kinesin; cytokine; interferon;
 KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
 KW multifactorial disease; autoimmune disease; infection;
 KW nervous system disease.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO200147944-A2.
 XX
 XX 05-JUL-2001.
 PD
 XX 28-DEC-2000; 2000WO-US35498.
 XX
 XX 28-DEC-1999; 99US-0173419.
 PR 27-DEC-2000; 2000US-0173419.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkets RA, Leach M;
 PI
 XX WPI: 2001-465210/50.
 DR
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g.
 PT cancer, autoimmune diseases and infections -
 XX
 XX Disclosure; Page 3997; 4143pp; English.
 PS
 XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
 CC system and an infection of pathogenic organisms.
 CC
 SQ Sequence 14 AA;
 Query Match 26.3%; Score 5; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 10 RGRTS 14
 3 RGRTS 7
 DB
 RESULT 15
 AAG66412
 ID AAG66412 standard; Peptide: 15 AA.
 XX
 AC AAG66412;
 XX
 XX 22-OCT-2001 (first entry)
 DT
 XX G2 peptide.
 DE
 XX
 XX G protein 44; cancer; HIV infection; cytostatic; anti-HIV; G2.
 KW
 XX Unidentified.
 OS
 XX CN1296958-A.
 PN 30-MAY-2001.
 XX
 PD 22-NOV-1999; 99CN-0124046.
 XX
 XX 22-NOV-1999; 99CN-0124046.
 PR
 XX (SHAN-) SHANGHAI BORONG GENE DEV CO LTD.
 PA
 XX

PI Mao Y, Xie Y;
 XX
 XX WPI: 2001-489557/54.
 DR
 XX
 XX Polypeptide-human G protein 44 and polynucleotide for coding
 PT polypeptide, useful for treating e.g. cancer and HIV infection, is
 prepared by DNA recombination -
 PS
 XX Disclosure: Page 2 (Disclosure); 34pp; Chinese.
 XX
 CC The present invention relates to human G protein 44 and its coding
 CC sequence (see AAH75817 and AAG66409). The G protein and its coding
 CC sequence are useful for treating e.g. cancer and HIV infection. The
 CC present peptide, G2 peptide, was used in the present invention.
 XX
 SQ Sequence 15 AA:

Query Match 26.3%; Score 5; DB 22; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Gaps 0;
 Matches 5; Conservative 0; Indels 0;
 QY 11 GRTSS 15
 |||||
 Db 9 GRTSS 13

RESULT 16

AA95915
 ID AAY95915 standard; Peptide: 18 AA.
 XX
 AC AAY95915;
 XX
 XX 20-NOV-2000 (first entry)
 DE Hypothetical signal region of GGBP.
 XX
 KW Goodpasture antigen binding protein; GGBP; autoimmune disease;
 KW apoptosis; cancer; tumour; diagnosis; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200050607-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 24-FEB-2000; 2000WO-IB00324.
 XX
 PF 24-FEB-1999; 99US-0121483.
 XX

(SANSU) SANSU J.

Saus J;

WPI: 2000-572094/53.

Novel Goodpasture antigen binding proteins useful for diagnosing and
 treating autoimmune disorders, tumor, and preventing cell apoptosis -
 Example 1; Page 31; 158pp; English.

XX This peptide represents a portion of a hypothetical polypeptide
 CC encoded by an open reading frame upstream of the human Goodpasture
 CC antigen binding protein (GGBP) gene. An mRNA editing process
 CC inserting a single bp (U) would generate an operative in-frame
 CC start site and an open reading frame of 743 residues containing
 CC an export signal immediately downstream of the edited Met.
 CC Polyclonal antibodies raised against the peptide displayed a
 CC linear vascular reactivity in human tissues suggestive of an
 CC extracellular basement membrane localisation. GGBP (see AAY95900)
 CC is a novel serine/threonine kinase that specifically binds to and
 CC phosphorylates the N-terminus of Goodpasture antigen. The
 CC invention provides nucleic acids (see AAY50341-53) encoding GGBP,
 CC recombinant vectors, host cells, encoded polypeptides (see

CC AAY95900-11) and antibodies. It also provides methods for detecting
 CC the presence of an autoimmune condition or apoptosis by detecting
 CC an increase in GGBP expression, and methods for treating an
 CC autoimmune disorder, apoptosis or a tumour by modifying GGBP
 CC expression or activity.
 XX
 SQ Sequence 18 AA:

Query Match 26.3%; Score 5; DB 21; Length 18;
 Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Gaps 0;
 Matches 5; Conservative 0; Indels 0;
 QY 11 GRTSS 15
 |||||
 Db 14 GRTSS 18

RESULT 17

AA847234
 ID AAB47234 standard; Peptide: 19 AA.
 XX
 AC AAB47234;
 XX
 XX 18-JUL-2001 (first entry)
 DE hMOF1 Mitofusin GTPase motif G1.
 XX

Mitofusin; homolog; GTPase; mediation; mitochondrial fusion; stroke;
 KW post-meiotic fusion; mitochondria; spermatid; anti-insect; deafness;
 KW antifungal; fertility; mortality; arthropod pest; Leigh's syndrome;
 KW mitochondrial disease; muscle myopathy; neurodegenerative disorder;
 KW aging; Alzheimer's disease; Parkinsonian's disease; cancer; psoriasis;
 KW autoimmune disease; diabetes mellitus; congenital muscular dystrophy;
 KW fatal infantile myopathy; mitochondrial encephalopathy; optic atrophy;
 KW lactic acidosis; mitochondrial diabetes; neuropathy; osteoarthritis;
 KW progressive external ophthalmoplegia; dystonia; schizophrenia.

Homo sapiens.

WO200125274-A1.

12-APR-2001.

06-OCT-2000; 2000WO-US27871.

06-OCT-1999; 99US-0413285.

(STPD) UNIV LELAND STANFORD JUNIOR.

Fuller MT, Hales KG, Santel AH;

WPI: 2001-300165/31.

New nucleic acid molecules encoding mitofusin polypeptides useful for
 identifying anti-insect, antifungal and therapeutic agents -
 Example 12; Page 51; 92pp; English.

XX The sequences given in AAB47231-45 represent the consensus sequences
 CC and homologs from the GTPase domains from some mitofusin proteins.
 CC Mitofusins are large predicted GTPases with a predicted transmembrane
 CC domain, coiled-coil region and a C-terminal region showing a high
 CC isoelectric point and a predicted coiled-coil region. They are
 CC the first known protein mediators of mitochondrial fusion, e.g.
 CC mediating developmentally regulated post-meiotic fusion of mitochondria
 CC in Drosophila spermatids. Mitofusin polypeptides are useful for
 CC enhancing membrane fusion in a population of membrane-bounded entities,
 CC e.g., mitochondria. Mitofusin proteins are useful for screening
 CC anti-insect or antifungal agents. Modulators of mitochondrial fusion
 CC are useful for reducing fertility and increasing the mortality rate
 CC of arthropod pest, e.g., an insect (claimed). Mitofusin DNA is
 CC useful for generating genetically modified non-human animals or
 CC site-specific gene modifications in cell lines, for the study of

CC mitofusin function or regulation, and to create animal models of
CC diseases, including mitochondrial diseases, muscle myopathies,
CC neurodegenerative disorders, and aging. Mitofusins, and the DNA
CC encoding them, can be used in assays to identify therapeutic agents
CC useful for treating chronic neurodegenerative diseases such as
CC Alzheimer's disease and Parkinson's disease, autoimmune diseases,
CC diabetes mellitus, congenital muscular dystrophy with mitochondrial
CC structural abnormalities, fatal infantile myopathy, mitochondrial
CC encephalopathy, lactic acidosis, stroke, mitochondrial diabetes,
CC deafness, neuropathy, progressive external ophthalmoplegia, optic
CC atrophy, Leigh's syndrome, dystonia, stroke, schizophrenia, progressive
CC joint disorders such as osteoarthritis, and hyperproliferative
CC disorders such as cancer, tumour and psoriasis.

XX Sequence 19 AA;

Query Match 26.3%; Score 5; DB 22; Length 19;

Best Local Similarity 100.0%; Pred. No. 1.7e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

11 GRTS 15
|||||
Db 7 GRTS 11

RESULT 18

AAR37218 AAR37218 standard; peptide; 10 AA.

XX AAR37218;

AC 06-SEP-1993 (first entry)

DE IL-6 antagonist peptide #2.

XX IL-6: antagonist; cytokine; B cell differentiation; inflammation;
XX tissue injury; B9.9 hybridoma cell line; Castleman's Disease;

XX Lemmink's T-cell lymphoma; Non Hodgkin's lymphoma; allergy;

XX Immune deficiency disease; cardiac myxoma;
XX mesangial proliferative glomerulonephritis.

XX US5210075-A.

XX 11-MAY-1993.

XX 16-FEB-1990; 90US-0480868.

XX 16-FEB-1990; 90US-0480868.

XX (TANA) TANABE SEIYAKU CO.

XX Chiang S, Lobl TJ, Nagarejan G, Scholz W;

XX WPI: 1993-166970/20.

XX New peptide interleukin-6 antagonists - for treating and
XX preventing auto-immune, immuno-inflammatory, neoplastic and
XX infectious diseases etc.

XX Claim 9; Column 27; 20pp; English.

XX This peptide is a specifically claimed example of a highly generic

XX Formula covering sequences derived from the p51-70 portion (i.e the

XX IL-6 receptor-binding portion) of IL-6 (see AAR37216) or modelled

XX after different portions of this sequence. In an assay to determine

XX IL-6 antagonist activity of this peptide, proliferation of the IL-6
XX dependent B9.9 hybridoma cell line (0. Immunol. 139: 4116, 1987) was
XX inhibited by 78 (+/-)9%.

XX See AAR37216-R37261.

XX Sequence 10 AA; Query Match 21.1%; Score 4; DB 14; Length 10;

Best Local Similarity 100.0%; Pred. No. 1.1e+03; Mismatches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 SKKE 17
|||||

Db 2 SKKE 5

RESULT 19

AAR63388 AAR63388 standard; Protein; 10 AA.

XX AAR63388;

XX 18-AUG-1995 (first entry)

DE Hepatitis C virus core protein polypeptide (variable region).

XX Hepatitis C virus; HCV; primer; probe; detection; diagnosis;

XX Classification; immunisation; prophylaxis; serotyping.

XX Hepatitis C virus.

XX WO9425601-A.

XX 10-NOV-1994.

XX 27-APR-1994; 94WO-EP01323.

XX 27-APR-1993; 93EP-0401099.

XX 05-AUG-1993; 93EP-0402019.

XX (INNO-) INNOGENETICS NV SA.

XX Maertens G, Stuyver L;

XX WPI: 1994-358277/44.

XX New polynucleotide sequences from hepatitis C virus - and related
XX vectors, polypeptide(s) and antibodies, useful for immunisation,
XX treatment, diagnosis and typing of HCV isolates

XX Claim 15; Page 272; 404pp; English.

XX Compositions comprising at least 5, and pref. 8 or more contiguous

XX nucleotides selected from an HCV type 3 genomic sequence, more

XX particularly (i) the region spanning positions 417-557 of the

XX Core/51 region of HCV subtype 3a; (ii) the region spanning positions

XX 4664-4730 of the NS3 region of HCV type 3; (iii) the region spanning

XX positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the

XX region spanning positions 8023-8235 of the NS5 region of the BR36

XX subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic

XX sequence, may be used as primers to amplify nucleic acid from an

XX isolate belonging to a specific genotype, or as a probe for specific

XX detection/classification of nucleic acid. Polypeptides encoded by

XX the nucleotides in such compositions may be used for immunisation

XX against HCV, for the detection of antibodies directed against HCV

XX (V-CORE) of HCV has been shown to be useful for serotyping.

XX Sequence 10 AA;

Query Match 21.1%; Score 4; DB 15; Length 10; Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GRTS 14
|||||

Db 4 GRTS 7

RESULT 20

AAR63389

ID	AAE63389	standard; Protein; 10 AA.
XX		
AC	AAE63389;	
XX		
DT	18-AUG-1995	(first entry)
XX		
DE	Hepatitis C virus core protein polypeptide (variable region).	
XX		
KW	Hepatitis C virus; HCV; primer; probe; detection; diagnosis;	
XX	Classification; Immunisation; prophylaxis; serotyping.	
OS	Hepatitis C virus.	
XX		
PN	MO9425601-A.	
PD	10-NOV-1994.	
XX		
PE	27-APR-1994;	94WO-EP01323.
XX		
XX	27-APR-1993;	93EP-0401099.
XX	05-AUG-1993;	93EP-0402019.
XX		
PA	(INNO-) INNOGENETICS NV SA.	
XX		
PI	Maertens G, Stuyver L;	
DR	WPI: 1994-358277/44.	
XX		
PT	New polynucleotide sequences from hepatitis C virus - and related	
XX	vectors, polypeptide(s) and antibodies, useful for immunisation,	
XX	treatment, diagnosis and typing of HCV isolates	
PS	Claim 15; Page 272; 404pp; English.	
XX		
CC	Compositions comprising at least 5, and pref. 8 or more contiguous	
CC	nucleotides selected from an HCV type 3 genomic sequence, more	
CC	particularly (1) the region spanning positions 417-957 of the	
CC	Core/E1 region of HCV subtype 3a; (1i) the region spanning positions	
CC	4664-4730 of the NS3 region of HCV type 3; (1ii) the region spanning	
CC	positions 4892-5292 of the NS3/4 region of HCV type 3; (iv) the	
CC	region spanning positions 8023-8235 of the NS5 region of the BR36	
CC	subgroup of HCV subtype 3a; or (v) an HCV subtype 3c genomic	
CC	sequence, may be used as primers to amplify nucleic acid from an	
CC	isolate belonging to a specific genotype, or as a probe for specific	
CC	detection/classification of nucleic acid. Polypeptides encoded by	
CC	the nucleotides in such compositions may be used for immunisation	
CC	against HCV, for the detection of antibodies directed against HCV	
CC	and for serotyping. The variable region in the core protein	
CC	(V-CORR) of HCV has been shown to be useful for serotyping.	
SO	Sequence	10 AA;
QY	Query Match	21.1%; Score 4; DB 15; Length 10;
Best Local Similarity	100.0%;	Pred. No. 1.1e+03;
Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	11 GRTS 14	
DB	4 GRTS 7	
RESULT 21		
AAW21262		
ID	AAW21262	standard; peptide; 10 AA.
XX		
AC	AAW21262;	
XX		
DT	29-JUL-1997	(first entry)
XX		
DE	Hydroxymethylglutaryl coenzyme A reductase signal oligopeptide #21.	
XX		
KW	Hydrophilic; signal oligopeptide; hydrophilicity maxima; vaccine; SIV;	
XX	competitive inhibitor; feedback regulator; synthesis; gastrin precursor;	
KW		

KW	charge; polarity; farnesyl synthetase; plasminogen activator inhibitor 1;
KV	hydroxymethylglutaryl coenzyme A reductase; glucagon precursor; rhesus;
KW	gonadolibetin precursor; Plasminogen activator inhibitor 2; proteinin;
KM	Alzheimer amyloid A4; corticotropin releasing factor binding protein;
KW	apolipoprotein E; herpes virus 1 glycoprotein B; HSV1; human; OMVS;
KM	herpes virus 2 glycoprotein B; HSV2; collagenase; apolipoprotein A;
KV	Trepone pallidum membrane protein; TMPA; Islet amyloid polypeptide;
KW	fibrinolytic MMP1; schistosoma elastase precursor; schistosomn;
KV	hepatitis delta antigen; rev protein; HIV; angiotensinogen.
XX	
OS	Homo sapiens.
PN	WO9519568-A1.
XX	
PD	20-JUL-1995.
XX	
PF	12-JAN-1995; 95WO-US00575.
XX	
PR	14-JAN-1994; 94US-0182248.
XX	
PA	(RATH/) RATH M.
XX	
PI	Rath M;
XX	
DR	WPI: 1995-263953/34.
XX	
PT	Identifying signal oligopeptide(s) in protein sequence(s) - shown as
PT	regions of max. hydrophilicity, used in modulating communication
PT	between protein(s)
XX	
PS	Claim 5; Page 33; 86pp; English.
XX	
CC	The sequences given in AAW21201-560 represent hydrophilic signal oligo-
CC	peptides. These signal oligopeptides are localised on the surface
CC	of the protein and are represented by the hydrophilicity maxima of
CC	the protein. These peptides are enriched in charged amino acids
CC	arranged with neutral spacer amino acids. The specific signal
CC	character of these oligopeptides is determined by a characteristic
CC	combination of conformation and charge within the signal sequence.
CC	These oligopeptides may be used as vaccines in the treatment of
CC	human disease, as competitive inhibitors to prevent or reduce the
CC	metabolic action or interaction of a selected protein by blocking
CC	its specific signal sequences, or as therapeutic agents to function
CC	as feedback regulators to reduce synthesis rate of a selected protein.
CC	These peptides may be modified by omitting one or more amino acids at
CC	the N- and/or C-terminal, by substituting one or more amino acids
CC	without consideration of charge and polarity, by substituting one or
CC	more amino acids with amino acid residues with similar charge and/or
CC	polarity, by omitting one or more amino acids or a combination of these.
XX	
SQ	Sequence 10 AA:
XX	
Query Match	21.1%; Score 4; DB 16; Length 10;
Best Local Similarity	100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	14 SSKE 17
DB	3 SSKE 6
XX	
RESULT 22	
AAW12579	
ID	AAW12579 standard; peptide; 10 AA.
XX	
AC	AAW12579;
XX	
DT	08-APR-1997 (first entry)
XX	
DE	SH2 binding peptide #9.
XX	
KW	Core peptide: src homology region 2 binding peptide; SH2; cell growth;
KW	differentiation; regulation; receptor tyrosine kinase pathway; Cancer;
KW	

KM		signal transduction pathway; non-insulin dependent diabetes;
XN		insulin-resistant diabetes.
XX	Synthetic.	
CS		
XX	Key	Location/Qualifiers
FH	Modified-site	4
FT	/label= OTHER	
FT	/note= "opt. phosphotyrosine"	
PX		
PN	M09623813-AI.	
XX		
FD	08-ANG-1996.	
XX		
PE	31-JAN-1996;	96WO-USO1544.
XX		
PR	01-FEB-1995;	95US-0382100.
XX		
PA	(AFFY-) AFFYMAX TECHNOLOGIES NV.	
XX	Gordeev MF, Gordon E, Grove JR, Hart CP, Kim MH,	
PI	Patel DV, Szardenings AK;	
XX		
DR	WPI: 1996-371373/37.	
XX		
PT	Peptide(s) which bind to SH2 domains - are used to treat diseases	
PF	associated with aberrant cell growth, differentiation or regulation	
PT	associated with defects in receptor tyrosine kinase pathways	
PS	Claim 8 and 13; Page 116-117; 203pp; English.	
XX		
CC	The sequences given in AAW12551-70 represent core peptides of an src	
CC	homology region 2 (SH2) binding peptide which correspond to the	
CC	formula:	
CC	Z7-X-Z8-X	
CC	X = any D- or L- amino acid;	
CC	Z7 = phosphotyrosine or its isostere;	
CC	Z8 = asparagine or its isostere; and the peptide is less than 14	
CC	residues in length, with the proviso that if Z7 is phosphotyrosine	
CC	and Z8 is asparagine, then the peptide is not GDDGZVZXKPLLL. SH2	
CC	binding peptides containing these core peptides are used to treat of	
CC	disease disorders associated with aberrant cell growth, differentiation	
CC	or regulation which is associated with defects in receptor tyrosine	
CC	kinase pathways, by partially blocking or inhibiting a cellular signal	
CC	transduction pathway. The disease may be cancer, a developmental or	
CC	differentiation disease or insulin-resistant (or non-insulin dependent)	
CC	diabetes.	
CX		
XX		
SQL	Sequence	10 AA;
OQ	Query Match	21.1%; Score 4; DB 17; Length 10;
BEST	Best Local Similarity	100.0%; Pred.No. 1.le+03;
Matches	4; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	I NVPIC 4 Db 6 NVPIC 9	
ID	AAY55308 standard; peptide; 10 AA.	
AC	AAY55308	
DF	07-JAN-2000 (first entry)	
DE	CD34 antigen antigenic peak peptide SEQ ID NO:202.	
XX		
KM	Antibody releasing peptide; CD34; hybridoma; binding; antigen; cell surface antigen; identification; hematopoietic stem cell; tumour; cancer; immune system; therapy; displacement.	
KW		

XX Synthetic.
OS Homo sapiens.
XX
XX US5968753-A.
XX
XX 19-OCT-1999.
XX
XX 07-JUN-1995; 95US-0482228.
XX
XX 14-JUN-1994; 94US-0259427.
XX
XX (NEXE-) NEXELL THERAPEUTICS INC.
XX
XX Guillermo R, Helgerson SL, Deans RJ, Tseng-Law J, Kobori JA;
PI Al-Abdaly FA;
XX
XX WPI: 1999-590399/50.
XX
XX Short peptides useful for displacing antibodies from cell surface
XX antigens.
XX
XX Example 11: Column 38; 81pp; English.
XX
XX The present invention describes peptides of 4-17 amino acids which
XX displace either the anti-CD34 monoclonal antibody designated 561, the
XX anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC
XX HB-11646 (designated 9069), the anti-CD34 antibody produced by
XX hybridoma ATCC HB-11885 (9079), or the anti-human breast cancer
XX antibody produced by hybridoma ATCC HB-11884 (9187), from a cell
XX surface antigen on a target cell. The peptides are useful for
XX displacing antibodies bound to cell surfaces to release cells that
XX have been positively selected by antibody-mediated binding to beads
XX or other solid support. AAY5107 to AAY5319 represent peptides used in
XX the exemplification of the present invention.
XX
SQ Sequence 10 AA;
XX
Query Match 21.1%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 13 TSSK 16
| | | |
DB 6 TSSK 9
XX
XX JULN 25
XX AAY06153 standard; Peptide; 10 AA.
XX
XX AAY06153;
XX
XX 16-AUG-1999 (first entry)
XX
XX scFv 9A4 clone 23A VH CDR3 region.
XX
XX
XX Type II collagen; assay; antibody; rheumatoid arthritis;
XX osteoarthritis; diagnosis; monoclonal antibody; Mab; scFv;
XX single chain antibody; complementarity determining region; CDR;
XX mutant.
XX
XX Mus musculus.
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX Misc-difference 2 /note= "Ala in native sequence"
XX Misc-difference 5 /note= "Gly in native sequence"
XX Misc-difference 10 /note= "unidentified residue"
XX

PN EP921395-A2.
XX
XX 09-JUN-1999.
XX
XX
XX 12-NOV-1998; 98EP-0309266.
XX
XX 13-NOV-1997; 97US-0065423.
XX
XX (PFIZ) PFIZER PROD INC.
XX
XX Downs JT, Johnson KS, Mezes FS, Otterness IG;
XX
XX WPI: 1999-315488/27.
XX
XX Monitoring biological media for collagen fragments, using capture
XX and/or detection antibodies
XX
XX
XX Example 8; Page 30; 64pp; English.
XX
XX This sequence represents the mutated complementarity determining
XX region CDR3 of the heavy chain variable region (VH) of single chain
XX antibody scFv 9A4 clone 23A. It has 2 amino acid changes from the
XX parent 9A4 VH CDR3 clone (see AAY06150). A library of 9A4 scFvs was
XX expressed in E. coli that carried mutated CDR3 sequences (see
XX AAY06151-81). Binding studies to a collagen fragment demonstrated
XX that changes could be made to the amino acid sequence of the parent
XX scFv (see also AAY06130) while still retaining binding to the target.
XX By altering different regions of 9A4 VH and VL, antibodies with
XX variable to enhanced binding properties relative to the parent
XX antibody can be produced. The invention provides a method for
XX monitoring biological media for collagen II fragments, using capture
XX and detection antibodies such as 9A4 and its engineered variants.
XX The method can be used to assess the breakdown of type II collagen
XX by collagenase in normal and pathological (rheumatoid arthritis,
XX osteoarthritis) conditions.
XX
SQ Sequence 10 AA;
XX
Query Match 21.1%; Score 4; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 GRGR 12
| | | |
DB 2 GRGR 5

Search completed: May 9, 2003, 16:05:27
Job time: 35 secs